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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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   IDENTITY_NUC Gapent 1.0
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### Result O O a a a o o O a a No. 133.6 133.6 133.6 133.6 133.6 133.6 59.8 59.8 50.4 50.2 50 49.8 49.4 57.2 56.8 55.4 54.8 53.4 51.6 51.6 51.2 49 49 Query 1141 0 112698 0 129096 0 245802 0 293431 .5 4102 .5 216508 .4 1141 .7 5420 .5 133501 8 185558 8 1686 8 135599 8 192581 7 6175 7 178098 7 178098 9 146383 9 82469 1055 29016 1324 4591 245802 349980 158094 60182 7175159 182025 146454 146454 144575 Length 914 DB AF056936 AC116956 AF270648 AL683805 AC119418 AC126019 AC006279 PFMAL13P4 PFRESA AX083744 I58290 I58297 SWPSPIH AR145576 AR145583 CPU30821 AX083744 SWPHLSB AF410153 AF410153 ALIGNMENTS SUMMARIES M69183 Plasmodium AL031749 Plasmodiu AC097877 Rattus no AL138900 Human DNA AX083745 Sequence AC117266 Dictyoste X05182 P.falciparu AC006279 Plasmodiu AX344559 Sequence AC118262 Rattus no AX083744 Sequence X55124 P.falciparu AX083744 Sequence AC119418 Medicago AC126019 Medicago AC006279 Plasmodiu AL049181 Plasmodiu AL049181 Plasmodiu AX281184 Sequence AC116367 Oryza sat AC116380 Dictyoste AF206632 Plasmodiu AC129389 Rattus no E08995 DNA encodin U30821 Cyanophora ALO49180 Plasmodiu AX346209 Sequence AC040955 Mus muscu 166494 Sequence 14 AF056936 Plasmodiu AC116956 Dictyoste AF270648 Plasmodiu AR145576 Sequence AR145583 Sequence I58290 Sequence 1 I58297 Sequence 14 L22013 Swinepox vi AJ293568 Yaba-like AR145601 Sequence I58315 Sequence 53 L21931 Swinepox vi Description AL683805 Mouse DNA AF410153 Swinepox AF410153 Swinepox

YDI293568 YDI293568 Yaba-like disease virus (YLDV), complete genome. AJ293568 AJ293568 AJ293568 AJ293568 AJ293568 1011 gene; 1012 gene; 1031 gene; 1041 gene; 1051 gene; 1061 gene; 1071 gene; 1081 gene; 1091 gene; 1107 gene; 1168 gene; 1117 gene; 1117 gene; 1118 gene; 1118 gene; 1118 gene; 1119 gene; 1119 gene; 1119 gene; 1110 ge			ACCESSION VERSION KEYWORDS	RESULT 1 YDI293568/c LOCUS DEFINITION
144575 bp DNA linear VRL 30-M asse virus (YLDV), complete genome.  [:12056159 L gene; 102R gene; 103L gene; 104L gene; 105L L gene; 108L gene; 109L gene; 10L gene; 11/3R LL gene; 119L gene; 114R gene; 115R gene; 121L g  [1 gene; 119L gene; 121R gene; 121L g  [2 gene; 119L gene; 125R gene; 127R g  [3 gene; 124R gene; 125R gene; 137R gene; 127R g  [4 gene; 124R gene; 136R gene; 137R gene; 147R g  [5 gene; 140R gene; 141R gene; 143R g  [6 gene; 146R gene; 147R gene; 148R gene; 149R g  [7 gene; 146R gene; 147R gene; 148R gene; 149R g	122R gene; 123 128L gene; 123 128L gene; 134 133L gene; 134 139R gene; 131 144R gene; 145	106L gene; 107 110R gene; 111	AJ293568 AJ293568.1 GI	YDI293568
DNA linear VRL 30-M complete genome.  103L gene; 104L gene; 105L; 109L gene; 11/3R; 114R gene; 115R gene; 11/3R; 114R gene; 126R gene; 127R; 125R gene; 126R gene; 127R; 136R gene; 137R gene; 137R gene; 137R gene; 137R gene; 137R gene; 137R gene; 147R gene; 147R gene; 148R gene; 149R; 149R gene; 149R	in gene; 124R gene gene; 121 gene; iR gene; 135R gene iR gene; 135R gene gene; 140R gene; iR gene; 146R gene;	7L gene; 108L gene LL gene; 112L gene	[:12056159	144575 bp
	; 114 gene; 1201 gene; 1211 g ; 125R gene; 126R gene; 127R 130L gene; 131R gene; 132R g ; 136R gene; 137R gene; 138R 141R gene; 142R gene; 143R g ; 147R gene; 148R gene; 149R	; 1031 gene; 1041 gene; 1051 ; 1091 gene; 101 gene; 11/3R ; 114R gene; 115R gene; 116R	. 1031 comp. 1047	Ħ

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AUTHORS
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thesis (2000) Sir William Dunn School of Pathology, University of Oxford, Oxford, UNITED KINGDOM
2 (bases 1 to 144575)
Lee,H.J., Essani,K. and Smith,G.L.
The genome sequence of Yaba-like disease virus, a yatapoxvirus Virology 281 (2), 170-192 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yaba-like disease virus
                                                                                                                                                                                                                                                        Submitted (13-JUL-2000) Lee H.J., Sir William Dunn School of Pathology, University of Oxford, South Parks road, Oxford, OX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                   Direct Submission
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   /db_xref="taxon:132475"
complement(755. .1756)
                                                                                                         /organism="Yaba-like disease virus"
                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                    University of Oxford,
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FEATURES

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AUTHORS

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/gene="1L"
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/gene="2L"
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/gene="2L"
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/gene="3L"
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pcetivleksertkgyfgavkrvlassitdynyvcehltivkcfkgvgydnrfsitf
edhhrgreytlylhissfrngktydvgydkyvisthadfalekrseglaksvyvgesk
edhhrgreytlyklskeadviftlarfskdvkfyekegdrnlcyalvevnspfaevesfgyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(3630. .4346)
/gene="4L"
/function="Unknown"
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lkilreefygcnvrliydiisivstkvckmikdennnllitsnylnkklnfikmnkvf
knnsiddiiyvyfnykknnnivscgkvfkelmkydeiakkqyqeklhkdinnfklnnk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="related to swinepox virus C5L and vaccinia virus strain Copenhagen K7R" \,
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/gene="3L"
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NTYSLTDLYRTTSKMSSQPYCYVFHDTLEAQVYTCSEGCNGELYDHLYRKTEEGEGEE
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LVTKISYNHETRHGNYNFRADWFNISRSPHTPGNDYNFNFWYSLMKETLEEINKNDST
KTTSLSLITGCYETGLLFGSYGYVETANGPLARYHTGDKRFTKWTHKGFPKVGMLTYK
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/db_xref="GI:12056161"
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/db_xref="GI:12056160"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="related to swinepox virus C5L and vaccinia virus
strain Copenhagen N2L"
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/db_xref="GI:12056162"
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/note="related to swinepox virus ClL and chicken MHC-I"
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SMSYVSNFNIMMKEYFSFRONNKNNNIHVGKIFREIMSYDELAINHYGOLYIKNAIIE
INSPRDSYSFSIYKRFKRKIDDTISVNIDFIKKIIGFISILSVHDTVYDSNPISYIFF
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2407

2347

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Matches 1003;
             2646 TAACTTTAACTTTTGGTATTCTTTAATGAAAGAAACTTTAGAAGAAATTAATAAAAACGA
                                                                                                                                                                                     247 CAACTITAACTITTGGTATTCTTTAATGAAAGAAACTTTAGAAGAAAATTAATAAAAACGA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 CATGAATAAGTTAATATTATTTAGCACAATTGTAGCAGTTTGTAACTGCATAACTTTAAA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                        TAGCACAAAAACTACTTCGCTTTCATTAATCACTGGGTGTTATGAAACAGGATTATTATT
                                                                                                          TAGCACAAAAACTACTTCGCTTTCATTAATCACTGGGTGTTATGAAACAGGATTATT 366
                                                                                                                                                                                                                                         TTACAACGATCAGTTAGTGACGAAAATATCATATAACCATGAAACTAGACACGGAAACGT
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                                                                                                                                                                                                                                                                                                                                                                                         ATATAATTATACTGTTACGTTAAAAGATGATGGGTTATACGATGGAGTATTTTACGATCA
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human CC chemokine receptor type 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(5433. .6488)
/gene="7L"
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complement(5433. .6488)
/gene="7L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:Q9DHY6"
/translation="MEECPGYCLVDCLNRDDDIRQIIVDYIYWSMYSYRSRSPAGKVF
OVLKMFRRDSEIVFGENFRHIVKNFKTLGIEDTVQAVKCFTLGKNALRESVSMVDLCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(4920. .5369)
/gene="6L"
complement(4920. .5369)
/gene="6L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="putative CC chemokine receptor"
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/protein_id="CAC21244.1"
/db_xref="GI:12056165"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="msdicwicondycderunecgcneeykyvhikcmolwinyskkke
CNLCKTKYNIKKTYYSFKKWNWCFNDKKTTLEKIFFILFALVFIFLTITLSNDMANLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="5L protein"
/protein_id="CAC21243.1"
/db_xref="GI:12056164"
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/gene="5L"
/function="Unknown"
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/gene="5L"
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35 TTACAGCATATGTAGATGCTTCCGCATTCTTAGTATACAATTATACATATACTTTACAAG
                                   27 TTAGCACAATTGTAGCAGTTTGTAACTGCATAACTTTAAAATATAATTATACTGTTACGT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  787 GCCAGGAGAGCCAGGTTTTCCATGGAATATTAAAAAAGATAAAGATGCAAACACATATAG
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Moyer,R.W., Vinuela,E. and Gibbs,E.P.J.
Use of recombinant swine poxvirus as a
Patent: US 6217882-A 53 17-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                 Unknown
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Sequence 53 from patent US
AR145601
                                                                                                    Similarity
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                                                                                                                                  Sequence 53 from patent US 5651972.
Unclassified.
1 (bases 1 to 1023)
                                      Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451;
                                                  861 TACGTACAACATCAAAAATGAGTAGTCAACTAGTATGTGTTTGTCTATGACACTTTAG
                                                                                                                                                                                                                    741 TTAACGGAAGATACTATCCAGAATGGGGGAGAAAATCCGATTATGAGCCAGGAGAGCCAG
                                                                                                                                                                                                                                                                                                                                      635 CAGGAATTGAAAGAGGAGA---TAATACTACATTGATATGCACATTTGATAATCATTATC
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                            866 TTATGGTACCAACTATCATGTCTAATAGAATAGCATGTGTTTGGATTTCATAGTACGTTAG
                                                                                                                                            801 GTTTTCCATGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGATTTAG
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Use of recombinant swine poxvirus as a live vaccine vector
Patent: US 5651972-A 53 29-UUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                      ATCCG-----TACGTAAATGAATTGCTTCCTGATACGGACTATCTACCGGGTGAACCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Massung, R.F., Jayarama, V. and Moyer, R.W.

DNA sequence analysis of conserved and unique regions of swinepox virus: identification of genetic elements supporting phenotypic observations including a novel G protein-coupled receptor homologue Virology 197 (2), 511-528 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-JUL-1993) Robert F. Massung, Centers for Disease Control and Prevention, MS G-18, 1600 Clifton Rd., NE, Atlanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massung, R.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Swinepox virus serine protease inhibitor (orf K1R) gen protein coupled receptor (orf K2R) gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Swinepox virus
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G protein-coupled receptor; serine protease inhibitor.
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/protein_id="AAC37874.1"
/db_xref="GI:347191"
/translation="MLSYIINPLLSIVYFILGNVSKLLTYILMXIMIFILRAVNPYSLISNRGWLSLDSINPFKKEKRRESFLSSLNPFRKEETKKKEGFFSGWFG"
2540. .3562
                                                                                                                                                                                                       PIKROPYRTKRIGILMCCSAWLLSLILSSPVSKLYENIPHMSKOTYOCTLTNENDSII
AFIKRLMQIETTILGFLIPIIIFVYCYYRIFTTVVRLRNRKYKSIKIVLMIVVCSLI
CWIPLYIVLMIATIVSLYTSNIFRHLCLYLNLAYAITFSETISLARCCINPIIYTLIG
                                                                                                                                                                                                                                                               /product="G protein-coupled receptor"
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SDCIFVFQIPFIYYSKLDQWIFGNILCKIMSVLYYYGFFSNNFIITLMSIDRYFAIVH
                                                                                                                                                                                           EHVRSRISSICSCIYRDNRIRKKLFSRKSSSSSNII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MDVFLKLLQKDGNIVYSPVSISLSIDMIISKKGYIHRPLSPYTN VNEDTISIASRIYDDONSLKKDPCICMDCIGDMFVLVDFDKNIKEDIIDDINKMYSERT NNHLDTIIDNIGDNTKLITVANAYKRSWEDEBIKETTSIBKEWYNSTEFILVPMASN KDIYSYGYIKDSDKILIEIPYKDRRFSMFIPITKVYKTLCNIITIDKLAMWTSTMNLY
                                                                                                  /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVDIKIPRFKVESSYELKDIIGCINMEYYIREGTELNTPSGFRHKSVIEVNEDGTTAS
                                                                                                                     /note="putative"
                                                                                                                                     /standard_name="K3R"
                                                                                                                                                  /function="homologue of Shope fibroma virus
                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name="orf K2R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASTCCCVADSVSNKEFYAYSPFIFYIKDNTTSDFLFVGKIISPM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="serine protease inhibitor"
/protein_id="AAC37872.1"
/db_xref="GI:347189"
                                                                                                                                                                                                                                                                                                                                                                                                            note="homologue; putative"
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                                                           801 GTTTTCCATGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGATTTAG 860
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                                                                                                                          ATCCG-----TACGTAAATGAATTGCTTCCTGATACGGACTATCTACCGGGTGAACCAG
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KLPETGNPYKTMSLTJCGTDLRQLQVNEGYVYKISKGYIDKPVKFFYKVTGLEGE
VGMLTYKSQHWERVMEHLGSMYTLTCPFTADDYYKISKGYIDKPVKFYTYTYTGLEGE
VGMLTYKSQHWERVMEHLGSMYTLTCPFTADDYKISKGYIDKPVKPYTYTYTGLEGE
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Moyer,R.W., Vinuela,E. and Gibbs,E.P.J.
Use of recombinant swine poxvirus as a live vaccine
Patent: US 6217882-A 1 17-APR-2001;
Location/Qualifiers
1. .14176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
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    AGACTATGTCCTTGACAATTGGATGTACTGATCTAAGACAACTTCAAGTAAATTTCGGTT 13542
                             ---CGCTTTCATTAATCACTGGGTGTTATGAAACAGGATTATTATTTGGTAGTTATGGGT 380
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13183 TTACAGCATATGTAGATGCTTCCGCATTCTTAGTATACAATTATACATATACTTTACAAG 13242
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                                                                                                                     13363 TTAATGAGACTAAGATTAGATATTATCCGAAAAATAATTATAATTTTATGTTCTGGCTAA 13422
                                                                                                                                                                                                                                              13303 GTTTAAAACTAAATAGCGAGACAGGAAGACCAGAATTAAGAAATGAACCACCAACATGGT
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Moyer, R.W., Vinuela, E. and Gibbs, E.P.J.
Use of recombinant swine poxvirus as a live vaccine vector
Patent: US 6217882-A 14 17-APR-2001;
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ATAGAATGAGTGAAACGCTAGATGAGATAAATAAACTTCCAGAAACGAGTAATCCTTACA
                                                         CTTTAATGAAAGAAACTTTAGAAGAAATTAATAAAAACGATAGCACAAAAACTACTT---
                                                                                                                                                                        TTAATATTTCTAGGAGTCCCCACACGCCAGGTAACGATTACAACTTTAACTTTTGGTATT
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Moyer, R.W., Vinuela, E. and Gibbs, E.P.J.
Use of recombinant swine poxvirus as a
Patent: US 5651972-A 1 29-JUL-1997;
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Sequence 1 from patent US 5651972.
I58290
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   ATGATAATCATCGATATGACTTCGAAGTCACCGATTATTTTAATGATATACTAATAAAAC
                              TAAAAGATAATGGGTTATACGATGGAGTATTTTACGATCATTACAACGATCAGTTAGTAA 146
                                                           TTACAGCATATGTAGATGCTTCCGCATTCTTAGTATACAATTATACATATACTTTACAAG
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                                                                                                                                   Score 133.6; DB 6; Pred. No. 5.7e-16;
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          1 (bases 1 to 14176)
Moyer,R.W., Vinuela,E. and Gibbs,E.P.J.
Use of recombinant swine poxvirus as a live
Patent: US 5651972-A 14 29-JUL-1997;
                                                                                                                                              Sequence 14 from patent US 5651972. I58297
                                                                                                  Unknown
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DNA sequence analysis of conserved and unique regions of swinepox virus: identification of genetic elements supporting phenotypic observations including a novel G protein-coupled receptor homologue virology 197 (2), 511-528 (1993)
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G protein-coupled receptor; interferon-gamma pseudoprotease; ribonucleotide reductase.
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Direct Submission
Direct Submission
Submitted (22-JUL-1993) Robert F. Massung, Centers for Disease
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Swinepox virus complete ORFS
1.22013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Swinepox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Swinepox virus (strain Kasza) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suipoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 14176)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 14176)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MKEINSLECQWESIDDNNDTTIIGDDIYEDYIISQIDIHQNWSP
DIRLIKFERKENKESFOKISDTEPANT
DIRLIKFERKENKESFOKISDTEPANT
DIRLIKFERKENKESFOKISDTEPANT
LOTTORET PERLEVUNLKGEDEKLIVCAWAMGLYKLTELM
RLYKRVLYBENKOYSPIDTTPASTIPEKLYKNULKGEDEKKLIVCAWAMGLYKLTELM
SNINVLNYFTHAFHFFEHEKRANYLYDBGNIIIFPALKESDEKTEVANIEGEKSIV
QYKKTIFANIETHEKRANYLYDBGNIIIFFSHEKSDEFTIKKKYTYVFBL
DIKACLNDEDESQVANIINKKIKNSLKIEHNWYYDFHFFIHTLLRTYPEIESDKEFSD
                                                                                                                                                                                                                                                                                                                                                                                /translation="menpyrintlynvfvervienlsiysipinstcgihigeikgtp
krcptkilnwcinbkelsfniliktlkdvfstlsgrekeelskeigidinndbryvp
eiirncssabdytniidtgltbygkciapybkgillojvnsgtabancymsinnsm
erridnaniynylnitnrpwfifsiiiialifvigicsikrrigikykygffly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLEDFIMCCTKNTCEKFRLKVSILHPISFLENLITKNIFSNWINGESC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAC37852.1"
/db_xref="GI:347467"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAC37851.1"
/db_xref="GI:347466"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    putative"
                                                                 translation="MGSCVSVKSISISMDTVSISSIDDEYYYNIKNKPIYVRKNSCS/STLESRYSTYSLESRYSTKSVYF"
                                                                                                                                                                                                                           GOLCICKINKYKYGYSVNIFYRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="ORF C19L; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="homologue of vaccinia virus ORF F9L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10276"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Swinepox virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                         /protein_id="AAC37853.1"
/db_xref="GI:347468"
                                                                                                                                                                                                                                                                                                                     /codon_start
                                                                                                                                                                                                                                                                                                                                          /note="ORF C18L; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'strain="Kasza"
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/db_xref="GI:347469"
                                                                                                                                                              /codon_start=
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/codon_start=1
                       /note="ORF C16L; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C20L; homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp DNA
C20L-C1L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of vaccinia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poxviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRL 17-DEC-1993
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GA

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/product="pseudoprotease"
/protein_id="AAC37860.1"
/db_xref="GI:347475"
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VTDICLMIPDKCYGRISPRSGLSLNYNIDIGGGVIDSDYRGE#GIVFINNGCSDFNI
KVGDRIAQIIFERVEYFIMEEVKCLEDTERGNSGFGSSGM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /proteIn_id="AAC37858.1"
/db_xref="GI:347473"
/translation="Marketty Interpression of the following of the
                                                                                                                                                                                          NSTYSILYWMYGNNYTFVEQLNSDHYKEKKYNSTEKNEHMYKLRTDLIIYNITSEMEM
                                                                                                                                                                     TKLTCVLSDIYTPIKASIILNNLWSCLNTTQV'
                                             /note="ORF C8L; putative"
                                                                          function="homologue of vaccinia virus ORF K3L"
                                                                                                                                        7895. .8155
                                                                                                                                                                                                                                                                                     /protein_id="AAC37862.1"
/db_xref="GI:347477"
                                                                                                                                                                                                                                                                                                                                                                                             /note="ORF C9L; putative"
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IKKRYCKDFNSYTCILEYDENKYIDNVHKEVISILLSDSRPSIKLAAISILSIIIDKL
ICRNIRIAKYIIDDIINIISEDGIYIILFLDEFDKYTDTRCRRKGLSMMIASIVTYYC
                                                                                                                                                                                                                       "translation="MNRNMWIVLSCVLYMIYICNGRDVLLYPPHKKINKVIVKCNGYT
                                                                                                                                                                                                                                                                                                                                                                    codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAC37861.1"
/db_xref="GI:347476"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORF C10L; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORF CllL; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAC37859.1"
/db_xref="GI:347474"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHPRKCPGVAIFKNRIYVVGGIGYDGPLKTVESWSPGEQOWREEVPLLQPRFNPGIIG
TDNDLYVVGGISEDDKTIEIYSYEENTWSIGNAMNYSHFGGCIAYHHGYIYMIGGLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MNKYNNYRAIYFLYKVILRIHNTEYISGT".QRSIQNITPTTSSY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORF Cl2L; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDNIHVFTMVEKYNPHSNKWTVEKSLPFPRFNSSLCIIEDSIAIIGWIYY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MEPILQESDSRFVIFPIKYHDIWKMYKQSVASFWTVEEVDLSKD
LDDWDKLTKDEKYFIKHILAFFASSDGIVNENLAERFYVDVQCSEARCFYGFQIAMEN
IHSEMYSLLIDTYVDDNIEKMHLFNAIETMECVKKKADWARKWISSNKVYGERVVAFA
AVEGIFFSGSFAAIFWIKKRGLMPGLTFSNELISRDEGLHCDFACLMFKHLLHPPSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ′codon_start≃1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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/note="ORF C13L; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFIVDIFRQIRTRCLQWTSRREFLQLDNMYYTNDSSVGVNTE
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/translation="MNTTTSQIIIDNDMSNEVGTIMVITLCLVTIVITCYLLLQLVRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="ribonucleotide reductase"
/protein_id="AAC37857.1"
/db_xref="GI;347472"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIHKNNIKIPYKVKVIRKRCSSSDDDVFI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 12.98;
Local Similarity 49.08;
13303 GTTTAAAACTAAATAGCGAGACAGGAAGACCAGAATTAAGAAATGAACCACCAACATGGT 13362
                                                                                                                                                         13243 ATGATAATCATCGATATGACTTCGAAGTCACCGATTATTTTAATGATATACTAATAAAAC 13302
                                                                                                                                                                                                                                                                                                                   13183 TTACAGCATATGTAGATGCTTCCGCATTCTTAGTATACAATTATACATATACTTTACAAG 13242
                                                                              147 CGAAAATATCATATAACCACGAAACTAGACACGGAAACGTAAATTTTAGGGCTGATTGGT 206
                                                                                                                                                                                                                                        87 TAAAAGATAATGGGTTATACGATGGAGTATTTTACGATCATTACAACGATCAGTTAGTAA 146
                                                                                                                                                                                                                                                                                                                                                                                             27 TTAGCACAATTGTAGCAGTTTGTAACTGCATAACTTTAAAATATAATTATACTGTTACGT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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FYNIENSDFIDKNNDEIYICADYDILYIILEFMYTGNIVLTKDNIELVIQVCDYLCID
SLIKICEEYICGIIDETNCIHLLNESDTYNLQRLREMSKWYLPKIINNNKLVVELDID
DMILIIKEIKYIACEYIVKKIILNWIVHKDERIIYTKKLMKHINDQDHYTSLSDIELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGGKDTNOYMTNIVEFWKPEWKSWYDGQHLCYPRCYMSLVDYNNEWYTIGGKRTSTT
DEFNIEMIVSDDAYEKLTDHSWAKLKOPPIAKSGISSIVYNDFIYCIGGRIDTEHISI
EHTNDVYIYSSRDDCWKYLSNYNVKRSFCLSCVFNNELYIIGGYNTNSVEKYNKLKNT
WKRLNDIPKFEECVNEASAIYL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MNSYIVIKNSLRDYRSGRIIRKYIRKLNKDEYKHECAVERLNVD
FSQDDKNPSRKEVIRIIDEEFNFCDLRLFYDIMTVVPNHMNVASIIYSEYEYLLKKSN
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YNDIINTYKEGDTISINIRLKCKDDIIKHCKSSIGMFAILSSKIIDVDEDVIFFSQIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="G protein-coupled receptor homologue"
/note="ORF C3L; putative"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNIRERIYDNKEHDVDISHNFIIMVGGKKIFNITAFNDLSNKKHIIDRYDDMFGCKTH
FSVYYLNSILYIIGGKKRGYFTKEVLSYNIKNKLMCYEPELNYFRYDTSVCVSNGMIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MHFIFIILSLSFVVNADVFPSSVTLSSNDFDTIIKWDNNVISYDVELMQYSHDEWRTVCTNSLGYCNLTNSDIDNDDETWVRFKYENKTSNBHNIGRVCEIV
QITSPIVNMTRDGSIILLDIHHPMTYDNQYYIYNNITLCGFEFIYEATFIINDTIIPY
SIDNQYCDDVHCLFYFISQEPVCVYVMGMEQYYEFGFKKTDNSTRVCVDGLIPRKIDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="g1:347479"
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TSKNDVSFKLYTMIFYLLPFVITCISFITLIVYLYKYCKISAKNNTYDTIYEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAC37867.1"
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/note="ORF C4L; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORF C5L; homologue of vaccinia virus ORF K7R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAC37863.1"
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/translation="MSTMNTLAFCYGLPNINDITQGIIFVRNNIFYSYLTDYAMEACI
_NYINIRADKIEDLKKSLVGKTISVRVIRVDVLKGYIDVSIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RYRLIFKKYLIQSLYLQ"
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/db_xref="GI:347481"
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/db_xref="GI:347480"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                         TITLE
JOURNAL
                                                                                                               AUTHORS
                                     MEDLINE
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11752168
2 (bacco
                                                                                                                                                                                                                                                                AF410153 146454 bp
Swinepox virus isolate 17077-99,
AF410153
                                   J. Virol.
21624277
                                           Afonso,C.L., Tulman, E.R., ..., Kutish,G.F. and Rock,D.L.
The genome of swinepox virus
J. Virol. 76 (2), 783-790 (2002)
                                                                                                                                                    Suipoxvirus.
                                                                                                                                                                    Viruses;
                                                                                                                                                                                      Swinepox virus.
Swinepox virus
                                                                                                                                                                                                                                                AF410153.1 GI:18448493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGITACTGTAGGTGGTAATATATGGACACGATTCGACCCCAAGAATAAACGCTTTAGTA 13602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGACTATGTCCTTGACAATTGGATGTACTGATCTAAGACAACTTCAAGTAAATTTCGGTT 13542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---CGCTTTCATTAATCACTGGGTGTTATGAAACAGGATTATTATTTGGTAGTTATGGGT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAGAATGAGTGAAACGCTAGATGAGATAAATAAACTTCCAGAAACGAGTAATCCTTACA 13482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTTAATGAAAGAAACTTTAGAAGAAATTAATAAAAACGATAGCACAAAAACTACTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGAATTGAAAGAGGAGA---TAATACTACATTGATATGCACATTTGATAATCATTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTATTATAAAATTTCTAAGGGATATATAGATAAGCCCAGTTAAGCCTACTGTTACAGTTA 13782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACGTGTTATGGAACATCTTGGATCAATGGTAACATTAACATGTCCGTTTACAGCGGATG 13722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAATGACACATAAAGGTTTTCCCCAAGGTTGGAATGTTAACTGTAAAAAAACACTCTTTGGA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTAGAAACGGCCAACGGACCGTTGGCCAGATACCATACAGGAGATAAAAGGTTTACGA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGCGCAAGTTTATACTTGT 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTTTCCATGGAATATTAAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGATTTAG 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCCG----TACGTAAATGAATTGCTTCCTGATACGGACTATCTACCGGGTGAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTCGTCGGTCGCTGTTAAATGGTATAACATCGAGGACTTTGCTCCGGACTATCGTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCTGACGTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAGGTGAATATAAATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGGTAATGAGTTAGAAGATGGTAACATGACTCTTGAATGCAGTGTAAATTCATTTTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGATGTAAAAAACTTATCTAGGCGGTTTTGAATACATGGGATGTTCATTAGCTATTTTAG
                                                                                                                                                                                                                                                                                                                                                                                                     AACCAAGCATATATAGATGT 14093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTATGGTACCAACTATCATGTCTAATAGAATAGCATGTGTTGGATTTCATAGTACGTTAG 14073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 146454)
                                                                                                                                 (bases 1 to 146454)
                                                                                                                                                                    dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                     complete genome.
                                                                                                                   Zsak, L., Osorio, F.A., Balinsky, C.,
                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                           VRL.
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Animal Disease Center, U.S. Dept. Agriculture, Agricultural
Research Service, P.O. Box 848, Greenport, NY 11944-0848, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Afonso,C.L., Tulman,E.R., Lu,2., Balinsky,C., Osorio,F.A., Zsak,L., Kutish,G.F. and Rock,D.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="isolated from domestic swine in Hartington, 
Nebraska on March 12, 1999" 
complement(284. .736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SPV002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus LSDV001 and vaccinia virus strain Copenhagen B15R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(284. .736)
                                                                                                                                                                                                                                                                                                                                                   /product="5PV002 hypothetical protein"
/protein_id="AAL69741.1"
/protein_id="AAL69741.1"
/db_xref="GI-184495"
/translation="MCALSTCTRNVFSGIWGFVRGIIVYIVKFIGFIIVFLKSFFQLL
IDNLARIFMLFIFYDRLLNVIITGIYNMINFPMKKFIAFLFGNENPFNDYDIVTKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus LSDV002'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(811. .1323)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARAASYWGGDERPTSASTKVLLLLKELLTDNELKFVKTAAIVRLKKYG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="metnylyrndfildnddittalldylymsclsyrhrdpagklfav
fesfkrdaefvfgeniigfvkymfldsihgfahsksmistmlkkenyirescavvgll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Swinepox virus"
/isolate="17077-99"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTETYKSCSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SPV002"
/note="identical to SPV149, similar to lumpy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="SPV001 A52R-like family protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="identical to SPV150, similar to lumpy skin disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SPV001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SPV00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10276"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SPV003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDMMICDVYKDKDKDKDNNNNDIKSSNKTDMNTYTDPAYDFQRVLNFITIPNPFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAL69740.1"
/db_xref="GI:18448494"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=
       complement(2821. .3630)
/gene="SPV005"
                                                                                                                                                                                                                                                    complement(2494. .2772)
                                                                                                                                                                                                                                                                                             complement(2494.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAL69742.1"
/db_xref="GI:18448496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SPV003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
                                             complement(2821. .3630)
/gene="spv005"
                                                                               ISNRGWLSLDSINPFKKEKRRESFLSSLNPFRKEETKKKEGFFSGWFG"
                                                                                                                                                                                                virus LSDV004"
                                                                                                                                                                                                                                                                          /gene="SPV004"
                                                                                                                                                                                                                                                                                                                   LEDEED"
                                                                                                                                                                                                                                                                                                                                   LGDKYLFTSSPRVMVPTIMSNRIACVGFHSTLEPSIYRCVNCSGPEPVLQYQGDRRND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="SPV003 MHC class I alpha chain-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="identical to SPV148"
                                                                                                   /protein_id="AAL69743.1"
/db_xref="GI:18448497"
/translation="MLSYIINPLLSIVYFILGNVSKLLTYILMKIMIFLLRAVNPYSL
                                                                                                                                                                                                                    /note="identical to SPV147, similar to
                                                                                                                                                                                                                                      /gene="SPV004"
                                                                                                                                                            'product="SPV004 hypothetical protein'
                                                                                                                                                                              codon_start=
                                                                                                                                                                                                                                                                                             .2772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2452)
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/translation="MDPVCWICKDDYSIEKNYCNCKNEYKVVHDECMKKWIQYSRERS
CKLCNKEYNIISVRKPFSQWVFSIKDCKKSAILYATLFLCTFIISLVLTRINITKIID
                                                                                                                                                                                                                                                                                                                                                             /translation="MHFIFIILSLSFVVNADVFPSSVTLSSNDFDTIIKWDNNVISYD
VELMQYSHDEWRTVCTNSLGYCNLTNSDIDNDDETWVRFKYENVTSNEHNIGRVCEIV
QITSPIVNMTRDGSIILLDIHHPMTYDNQYYIYNNITLCGFEFIYEATFIINDTIIPY
SIDNQYCDDVHCLFYFISQEPVCVYVMGMEQYYEFGFKKTDNSTRVCVDGLIPRKIDT
                      TSKNDVSFKLVTMVFYLLPFVITCISFITLIVYLYKYCKISAKNNTYDTIYEL.
                                                                                                                                                                                                                                         complement(6918. .7385)
/gene="SPV009"
                                                                                                                                                                                                                                                                                              /gene="SPV009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YNDIINTYKEGDTISINIRLKCKDDIIKHCKSSIGMFAILSSKIIDVDFDVIFFSQIS
IRYRLLIFKKYLLOSLYLO"
COmplement (6061. .6885)
                                                                                                           /product="SPV009 LAP/PHD-finger-like protein"
/protein_id="AAL69748.1"
/db_xref="GI:18448502"
                                                                                                                                                                                                                                                                                                                                       YFIKDFDDIDRVNNRLYRVVSDKYESNISSKFMHLYNNILSSFKLILQELMVNTEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="SPV008 interferon gamma receptor-like protein"
/protein_id="AAL69747.1"
/db_xref="GI:18448501"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccinia virus strain
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FKODDKNPSRREVIRIIDEEFNFCDLRLFYDIMTVVPNHMNVASIIYSEYEYLLKKSN
YKNKKINYTILDKINNYHSIDDIIFMYLHWRKKYNNTCACGKLFKELMKYDILATKYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ygene="SPW007"
/fore="similar to lumpy skin disease virus LSDV009
/note="similar to lumpy skin disease virus LSDV009
raccinia virus strain Copenhagen K7R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYNIENSDFIDKNNDETYICADYDILYIILEFMYTGNIVLTKUNIELVIQVCDYLCID
SLIKICEEYICGIIDETNCIHLLNESDTYNLQRLREMSKWYLFKIINNNKLYVELDID
DMILIIKEIKYIACEYIVKKIILNWIDHKDERIIYTKKLMKHINDQDHYTSLSDIELY
NNIRERIYDNKEHDVDISHNEIIMVGGKKIFNITAFNPLSNKKHIIDRYDDMFGCKTH
                                                                                                                                                                                                      note="similar to lumpy skin disease virus LSDV010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to lumpy skin disease virus LSDV008 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5328. .6038)
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SIGGKDTNGYMTNIVEFWKPEWKSWYDGQHLCYPRCYMSLVDYNNEVYTIGGLKTSIT
                                                                                                                                                                                           codon_start=1
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/protein_id="AAL69745.1"
/db_xref="GI:18448499"
/translation="MNSLLIRLHDFFKHGIMCDIKIVSIENNKTISAHRLILSMYSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to lumpy skin disease virus vaccinia virus strain Copenhagen A55R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIYQCTLTNENDSIIAFIKRLMQIEITILGFLIPIIIFVYCYYRIFTTVVRLRNRKY
KSIKIVLMIVVCSLICWIPLYIVLMIATIVSLYTSNIFRHLCLYLNLAYAITFSETIS
LARCCINPIIYTLIGEHVRSRISSICSCIYRDNTIRKKLFSRKSSSSSNII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SPV008"
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/db_xref="GI:18448500"
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IITLMSIDRYFAIVHPIKRQPYRTKRIGILMCCSAWLLSLILSSPVSKLYENIPHMSK
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/protein_id="AAL69744.1"
/db_xref="GI:18448498"
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/codon_start=1
                                                                                                                                                                                                                                                                                                                      lement(6918. .7385)
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144457 AAGTTAGATCACGTACATTTCCAAAGGTAGGAATGTTAACTGTTAAATCACAACACTGGG 144516
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                                                    441 AAATGACACATAAAGGTTTTCCCCAAGGTTGGAATGTTAACTGTAAAAAAACACTCTTTGGA 500
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                                                                                                     ATGTTACTGTAGGTGGTAATATATGGACACGATTCGACCCCAAGAATAAACGCTTTAGTA 144456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTTAAAACTAAATAGCGAGACAGGAAGACCAGAATTAAGAAATGAACCACCAACATGGT 144216
                                                                                                                                                       ATGTAGAAACGGCCAACGGACCGTTGGCCAGATACCATACAGGAGATAAAAGGTTTACGA 440
                                                                                                                                                                                                                                                       ATAGAATGAGTGAAACGCTAGATGAGATAAATAAACTTCCAGAAACGAGTAATCCTTACA 144336
                                                                                                                                                                                                                                                                                                                                                                  CTTTAATGAAAGAAACTTTAGAAGAAATTAATAAAAACGATAGCACAAAAACTACTT--- 323
                                                                                                                                                                                                                                                                                                                                                                                                                    TTAATGAGACTAAGATTAGATATTATCCGAAAAATAATTATAATTTTATGTTCTGGCTAA 144276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAATATTTCTAGGAGTCCCCACACGCCAGGTAACGATTACAACTTTAACTTTTGGTATT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGATAATCATCGATATGACTTCGAAGTCACCGATTATTTTAATGATATACTAATAAAAC 144156
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                                                                                                                                                                                                                 AGACTATGTCCTTGACAATTGGATGTACTGATCTAAGACAACTTCAAGTAAATTTCGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAAAGATAATGGGTTATACGATGGAGTATTTTACGATCATTACAACGATCAGTTAGTAA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTACAGCATATGTAGATGCTTCCGCATTCTTAGTATACAATTATACATATACTTTACAAG 144096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="SPV012 putative integral membrane protein,
apoptosis regulator"
/protein_id="AAL69751.1"
/db_xref="GI:18448505"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICRNIRIAKYIIDDIINIISEDGIYIILFLDEFDKYTDTRCRRRGLSMMIASIVTYYC
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TKLTCVLSDIYTPIKASIILNNLWSCLNTTQV"
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LNYINTRADKIEDLKKSLVGKTISVRVIRVDVLKGYIDVSIV"
complement(7742. .8146)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to lumpy skin disease virus LSDV017"
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/product="SPV011 putative interleukin-18 binding protein"
/protein_1d="AAL69750.1"
/db_xref="GI:18448504"
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/db_xref="GI:18448503"
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                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144577 ATTATTATAAAATTTCTAAGGGATATATAGATAAGCCAGTTAAGCCTACTGTTACAGTTA 144636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF410153 146454 bp
Swinepox virus isolate 17077-99,
AF410153
                                                                                                                                                                                                                                                                                                Submitted (09-AUG-2001) African Swine Fever Research, Plum Island Animal Disease Center, U.S. Dept. Agriculture, Agricultural Research Service, P.O. Box 848, Greenport, NY 11944-0848, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Swinepox virus.
                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                Afonso, C.L., Tulman, E.R., Kutish, G.F. and Rock, D.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Afonso,C.L., Tulman,E.R., Lu,Z., Zsak,L., Osorio,F.A., Kutlsh,G.F. and Rock,D.L.
The genome of swinepox virus
J. Virol. 76 (2), 783-790 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suipoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF410153.1 GI:18448493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCAAGCATATATAGATGT 144947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCGCAAGTTTATACTTGT 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCG-----TACGTAAATGAATTGCTTCCTGATACGGACTATCTACCGGGTGAACCAG 144807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAACGGAAGATACTATCCAGAATGGGGGAGAAAATCCGATTATGAGCCAGGAGAGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTCGTCGGTCGCTGTTAAATGGTATAACATCGAGGACTTTGCTCCGGACTATCGTTATG 144753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCTGACGTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAGGTGAATATAAATATG 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGAATTGAAAGAGGAGA---TAATACTACATTGATATGCACATTTGATAATCATTATC 144693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGGTAATGAGTTAGAAGATGGTAACATGACTCTTGAATGCAGTGTAAATTCATTTTACC 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACGTGTTATGGAACATCTTGGATCAATGGTAACATTAACATGTCCGTTTACAGCGGATG 144576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGATGTAAAAACTTATCTAGGCGGTTTTGAATACATGGGATGTTCATTAGCTATTTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTATGGTACCAACTATCATGTCTAATAGAATAGCATGTGTGGATTTCATAGTACGTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACGTACAACATCAAAAATGAGTAGTCAACTAGTATGTGTTTTTCCATGACACTTTAG 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTTTCCATGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGATTTAG 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTACCAMAMATGGCTAMAGGTGAMATACCAMAGATACAMCACCTACAGTGAMAGTAM
                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 146454)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 146454)
                                                       complement(284. .736)
/gene="SPV001"
                                                                                                 complement(284. .736)
/gene="SPV001"
                                                                                                                                              /note="isolated from domestic swine in Hartington,
Nebraska on March 12, 1999"
                 /note="identical to SPY150, similar to lumpy skin disease virus LSDV001 and vaccinia virus strain Copenhagen B15R"
                                                                                                                                                                                                         /organism="Swinepox virus"
/isolate="17077-99"
                                                                                                                                                                                                                                                                            Location/Qualifiers
/codon_start=1
                                                                                                                                                                                        /db_xref="taxon:10276"
                                                                                                                                                                                                                                                                                                                                                                                                      Tulman,E.R.,
                                                                                                                                                                                                                                                                                                                                                                                                      Lu, Z., Balinsky, C., Osorio, F.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRL 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Balinsky,C
                                                                                                                                                                                                                                                                                                                                                                                                           Zsak,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         800
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complement(811. .1323)
/gene="SPV002"
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/protein_id="AAL69740.1"
/db_xref="GI:18448494"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virus LSDV002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="SPV003 
P32231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1430.
/gene="SPV003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="SPV002 hypothetical protein"
/protein_id="AAL69741.1"
/db_xref="GI:18448495"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(811. .1323)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="metnyiyrndeldnddittalldylywsclsyrhrdpagklfav
fesfkrdaefyfgeniigfykymfldsihgfahsksmistmlkkenyirescavygll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus LSDV004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2494. .2772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLPETSNPYKTMSLTIGCTDLRQLQVNEGYVTVGGNIWTREDPKNKRFSKVRSRTFPK
VGMLTVKSQHWERVMEHLGSMVTLTCPFTADDYYKISKGYIDKPVKPTVTVTGIERGD
NTTLICTFDNHYPSSVAVKWYNIEDFAPDYRYDPYVNELLPDTDYLPGEPGYPTITRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNDILIKRLKLNSETGRPELRNEPPTWFNETKIRYYPKNNYNFMFWLNRMSETLDEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTETYKSCSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDMMICDVYKDKDKDKDNNNNDIKSSNKTDMNTYTDPAYDFQRVLNFITIPNPFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MCALSTCTRNVFSGIWGFVRGIIVYIVKFIGFIIYFLKSFFQLL
IDNLARIFMLFIFYVDRLLNVIITGIYNMIMFPMKKFIAFLFGNFNPFNDYDIVTKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SPV002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARAASYWGGDERPTSASTKVLLLLKELLTDNELKFVKTAAIVRLKKYG'
                                                                                                                                          complement(3693. .5285)
/gene="SPV006"
                                                                                                                                                                                                                                                                                     DIYQCTLINENDSIIAFIKRLMQIEITILGFLIPIIIFVYCYYRIFTTVVRLRNRRKY
KSIKIVLMIVVCSLICWIPLYIYLMIATIVSLYTSNIFRHLCLYLNLAYAITFSETIS
                                                                                                                                                                                                                                                                                                                                                                                                          /product="SPV005 G protein-coupled CC chemokine receptor-like protein" /protein_id="AAL69744.1" /db_xref="GI:18448498"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SPV005"
complement(2821. .3630)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MLSYIINPLLSIVYFILGNVSKLLTYILMKIMIFLLRAVNPYSL
ISNRGWLSLDSINPFKKEKRRESFLSSLNPFRKEETKKKEGFFSGWFG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="SPV004 hypothetical protein"
/protein_id="AAL69743.1"
/db_xref="GI:18448497"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2494. .2772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEDEED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGDKYLFTSSPRVMVPTIMSNRIACVGFHSTLEPSIYRCVNCSGPEPVLQYQGDRRND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="identical to SPV148"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SPV003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="identical to SPV149,
                                                                                                                                                                                                                                    complement(3693.
                                                                                                                                                                                                                                                                LARCCINPITYTLIGEHVRSRISSICSCIYRDNTIRKKLFSRKSSSSSNII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="identical to SPV147, similar to lumpy skin disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SPV004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SPV004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:18448496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAL69742.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=
/product="SPV006 kelch-like protein"
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                                                                                    vaccinia virus strain Copenhagen A55R"
                                                                                                                                                                                                   /gene="SPV006"
                                                                                                                                                                                                                                                                                                                                                    /translation="MSDCIFVFQIPFIVYSKLDQWIFGNILCKIMSVLYYVGFFSNMF
IITLMSIDRYFAIVHPIKRQPYRTKRIGILMCCSAWLLSLILSSPVSKLYENIPHMSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to lumpy skin disease virus LSDV011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MITKAIVILSIITAYVDASAFLVYNYTYTLQDDNHRYDFEVTDY/
                                                                                                               note-"similar to lumpy skin disease virus LSDV151 and
                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHC class I alpha chain-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2452)
                                                                                                                                                                                                                                    .5285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .3630)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similar to lumpy skin disease
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gene

CDS

gene

SGC

gene

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/protein_id="AAL69747.1"
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/translation="MHFIFIILS"
/translation="MHFIFIILS"
/translation="MHFIFIILS"
/translation="MHFIFIILS"
/translation="MHFIFIILS"
/translation="MHFIFI
                                                                                                                                                                                                                                                                                               /product="SPV010 eIF2 alpha-like PKR inhibitor"
/protein_id="AAL69749.1"
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/tanslation="MSTMNTLAFCYGLPNINDITQGIIFVRNNIFYSYLTDYAMEACI
LNYINIRADKIEDLKKSLVGKTISVRVIRVDVLKGYIDVSIV"
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complement(7445. .7705)
/gene="SPV010"
/note="similar to lumpy skin disease virus LSDV014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(6918..7385)
/gene="SPV009"
complement(6918..7385)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:18448499"
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DMILIIKEIKYIACEYIVKKIILNWIDHKDERIIYTKKLMKHINDQDHYTSLSDIELY
                                                                                                                                                                                                                                                                    complement(7742. .8146)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSKNDVSFKLYTMVFYLLPFVITCISFITLIVYLYKYCKISAKNNTYDTIYEL" complement(7445. .7705)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SPV008"
/note="similar to lumpy skin disease virus LSDV008
vaccinia virus strain Copenhagen B8R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(6061..6885)
/gene="SPV008"
complement(6061..6885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNSYIVIKNSLRDYRSGRIIRKYIRKLNKDEYKHFCAVFRLNVD
FSQDDKNPSRKEVIRIIDEEFNFCDLRLFYDIMTVVPNHMNVASIIYSEYEYLLKKSN
YKNKKINYTILDKINKYHSIDDIIFMYLHWRKKYNNTCACGKLFKELMKYDILATKYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene-"Spy007"
/gene-"similar to lumpy skin disease virus LSDV009 and
/note-"similar to lumpy skin disease virus LSDV009 and
vaccinia virus strain Copenhagen K7R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFNIEMIVSDDAVEKLTDHSWMKLKQFPIAKSGISSIVYNDFIYCIGGRIDTPHISI
EHTNDYYIYSSRDDCWKYLSNINVKRSFCLSCVFNNELYIIGGYNTNSVEKYNKLKNT
WKRLNDIPKFEECVNEASAIYL
       /product="SPV011 putative interleukin-18 binding protein"
/protein_id="AAL69750.1"
                                                                                                                                                                                          complement(7742. .8146)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccinia virus strain Copenhagen K3L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MDPVCWICKDDYSIEKNYCNCKNEYKVVHDECMKKWIQYSRERS CKLCNKEYNIISVRKPFSQWVFSIKDCKKSAILYATLFLCTFIISLVLTRINITKIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="SPV009 LAP/PHD-finger-like protein"
/protein_id="AAL69748.1"
/db_xref="GI:18448502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNIRERIYDNKEHDVDISHNEIIMVGGKKIFNITAFNPLSNKKHIIDRYDDMFGCKTH
FSVVYLNSILYIIGGKKRGYFTKEVLSYNIKNKLMCYEPELNYFRYDTSVCVSNGMIY
                                                                             /codon_start=1
                                                                                                                note="similar to lumpy skin disease virus LSDV015"
                                                                                                                                                           /gene="SPV011"
                                                                                                                                                                                                                                 /gene="SPV011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRYRLIFKKYLIQSLYLQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YNDIINTYKEGDTISINIRLKCKDDIIKHCKSSIGMFAILSSXIIDVDFDVIFFSQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="SPV007 A52R-like family protein"
/protein_id="AAL69746.1"
/db_xref="GI:18448500"
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                                                                                                                                                                      CTCCTGACGTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAGGTGAATATAAATATG
                                                                                                                                                                                                                               CAGGAATTGAAAGAGGAGA---TAATACTACATTGATATGCACATTTGATAATCATTATC
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                                                                                                              CGTCGTCGGTCGCTGTTAAATGGTATAACATCGAGGACTTTGCTCCGGACTATCGTTATG
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/protein_id="AAL69751.1"
/db_xref="GI-18448505"
/translation="MYKKYNSNYCIRNYLYVYLKYNTINKLSRYERMIYTKIKNQCEA
IKYRYCNDFNSYTCILEYDENKYIDNYHKEVISILLSDSRPSIKLAAISLLSIIIDKL
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unclassified.
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                                                                                                                                                                 GCGCAAGTTTATACTTGTTCTGAAGGATGCAATGGAGAGCTATACGACCACCTATATAGA 982
                                                                                                                                                                                                               CGTACAACATCAAAAATGAGTAGTCAACTAGTATGTGTTGTTTTCCATGACACTTTAGAA
                                                                                                                                                                                                                                       CCTGACGTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAGGTGAATATAAATATGTT
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                                                                                                                    AAAACAGAAGAAGGAGAAGGTGAAGAGGATGAAGAAGACGGAAACCCTCGA 1033
                                                                                                                                                                                                                                                                                                   AACGGAAGATACTATCCAGAATGGGGGAGAAAATCCGATTATGAGCCAGGAGAGACCAGGT
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Kun,J.F., Waller,K.L. and Coppel,R.L.
Plasmodium falciparum: structural and functional domains
mature-parasite-infected erythrocyte surface antigen
Exp. Parasitol. 91 (3), 258-267 (1999)
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/note="MESA; PfEMP2"
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join(<1...150,281...>!
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Query Match Best Local Similarity

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                                                                                                                                                                                      Submitted (04-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   559 AGATTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGATACAACACCTACAGTGAAAGT 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 133501)
Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                           The Dictyostelium Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum chromosome 2 map 1512060-1645559 strain ... Ax4, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC116956.1 GI:19919988
                                                                                                       jency : Deutsche Forschungsgemeinschaft (DFG).
MOTE: This is a 'working draft' sequence.
This sequence will be replaced
                                                              by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTAGTACGTACAACATCAAAAATGAGTAGTCAACTAGTATGTGTTGTTTTCCATGACAC 915
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    ∕organism="Dictyostelium discoideum"
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                                                     96559 ТТААЛАТААТТАЛАЛАЛАЛАЛА 96538
                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                    96737 ТАССТТАТТС--СТААЛТТААЛААЛААСЛАЛАТААТАЛАЛАТААЛАЛТАЛАЛАТАЛТАЛАЛА 96680
                                                                                                                                                                                                                                                                                                                                                                                     96797 TGAAAAGGTATTTTTTTTTAACTTTTAAAAAGAAACATGTCATACAATAAAATTTTATT 96738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96975 АЛЛААЛАЛТААЛСАЛАЛТААЛАЛАДАДДДДТТСССАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛ
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                                                                                                                                                                      797 CCAGGTTTTCCATGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGAT 856
                                                                                                857 TTAGTACGTACAACATCAAAAA 878
                                                                                                                                                                                                                                                           737 TATGTTAACGGAAGATACTATCCAGAATGGGGGAGAAAATCCGATTATGAGCCAGGAGAG 796
                                                                                                                                                                                                                                                                                                                                            677 TACCCTCCTGACGTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAGGTGAATATAAA 736
                                                                                                                                                                                                                                                                                                                                                                                                                               617 GTAACGGGTAATGAGTTAGAAGATGGTAACATGACTCTTGAATGCAGTGTAAATTCATTT 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              557 TTAGATTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGATACAACACCTACAGTGAAA 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497 TGGAAAGATGTAAAAACTTATCTAGGCGGTTTTGAATACATGGGATGTTCATTAGCTATT 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       437 ACGAAAATGACACATAAAGGTTTTCCCCAAGGTTGGAATGTTAACTGTAAAAAAACACTCTT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377 GGGTATGTAGAAACGGCCAACGGACCGTTGGCCAGATACCATACAGGAGATAAAAGGTTT 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 GCTGATTGGTTTAATATTTCTAGGAGTCCCCCACACGCCAGGTAACGATTACAACTTTAAC 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 TTTTGGTATTCTTTAATGAAAGAACTTTAGAAGAAATTAATAAAAACGATAGCACAAAA 316
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Similarity 44.0%;
79; Conservative
                                                                                                                                /chromosome="2"
/map="1512060-1645559"
50753 a 15240 c 15399 g 51959 t
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/db_xref="taxon:44689"
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                                                    y Match 5.5%;
Local Similarity 46.7%;
hes 217; Conservative
559 AGATTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGATACAACACCTACAGTGAAAGT 618
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 4102)
Shan,Z.X., Yu,X.B., Fang,J.M., Li,X.R., Ma,C.L. and Wu,Z.D.
Cloning and expression of the mature parasite-infected erythrocyte
surface antigen gene of Plasmodium falciparum isolate FCC1/HN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF270648 4102 bp DNA linear INV 12-JUN-2000 Plasmodium falciparum mature parasite-infected erythrocyte surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-MAY-2000) Department of Parasitology, Sun Yat-Sen University of Medical Sciences, 74 Zhongshan Road II, Guangzhou, Guangdong 510089, P.R.China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF270648.1 GI:8468620
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/db_xref="GI:8486621"
/translation="MyTCRNLCYDKKNNMMENEGNKVKKYYNNSSLKKYMKFCLCTI
/translation="MyTCRNLCYDKKNNMMENEGNKVKKYYNNSSLKKYMKFCLCTI
ICYFLLDIYTMCESPTYSYSSIKNNNDRYVRILSETEPPMSLEEIMRTFDEDHLYSIR
ICYFLLDIYTMCESPTYSYSSIKNNNDRYVRILSETEPPMSLEEIMRTFDEEDHLYSIR
ICYFLLDIYTMGSVYTDKRNNCLQHIKLLEMQASERRKQQEEENAKDIEEI
NYIECLKNAPYIDDPLWGSVYTDKRNNCLQHIKLLEMQASERRKQQEEENAKDIEEI
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KKQVEDGIKENDTEGNDKVKGPEIITEEVKEEIKKQVEEGIKENDTEGNDKVKGPEIIT
TEEVKEEIKKQVEEGIKENDTESKDKLIGQEIITEEVKEGIKENDTEKSTIGGEIIT
TEEVKEEIKKQVEEGIKENDTESKDKLIGQEVIIEBVKVIKKVEKGIKENHTESKD
KVIGQEIIVEEVKEEIEKQVEEGIKENDTESKDKVIGQEVIKGDVNEBGPENKDKVK
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KKKKKSFFQMLGCNFLCNKNIETDDEEETLYVKDDAKRKHKFLREANTEKNDNEKKDK
LLGEGDKEDVKEKNDEQKDKVLGEGDKEDVKEKNDDQKDKVLGEGDKEDVKEKNDGKK
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/isolate="FCC1/HN"
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SKEHNTLNTFPNMALNEDFRREFHN I LS I HEDTDLMELKRI LYNLFLEYNPHMNNKQK
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EKEEVKEVKEKDTVNKDKVIGQEVIIEEVKEEVKKRVKKRNNKNENKDNVIVQEIMNE
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TGESKETGESKETGESKETGESKETGESKETGESKETGESKETGESKYTRIY
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Search completed: June 15, 2003, 21:11:31 Job time: 2752 secs

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and is derived Pred. No. is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.

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Tanapox virus (TPV Yaba-like disease Yaba monkey tumor Swinepox virus (C1 Swinepox virus Hin Nucleotide sequenc Reverse complement Yaba monkey tumor Human polynucleoti	Description

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ABL32324	ABL14832	ABL19707	ABL19706	AAX99554	AAX99539	AAA70106	AAT67161	AAL38336	ABQ69245	ABQ67197	ABK31495	ABL70468	ABL33464	AAX99678	ABQ67695 .	ABQ69391	AAA70236	ABL34142	ABL32976	AAA70189	ABK28166	AAS45325	ABL34155	AAA70212	AAX99653	AAS90685	AAA70099	AAH24065	ABK31370	AAS61274	ABL70327	AAT05868	AAN60472	ABL33307	AAQ87587
Human immune syste		Drosophila melanog	Drosophila melanog	Nucleic acid seque	Nucleic acid segme	Plasmodium falcipa	Plasmodium falcipa	Genomic sequence e	Listeria innocua D	Listeria innocua c	Signal transductio	Chemically treated	Hijman immino syste	Nucleic acid segue	Listeria innocua D	Listeria innocua D	Plasmodium falcipa	Human immune syste	Human immune syste	Plasmodium falcipa	DNA transcription	Chemically pretrea	Human immune syste	Plasmodium falcina	Nucleic acid seque	DNA encoding novel	Plasmodium falcipa	Yeast AOD9604-asso	Signal transductio	Human gene regulat	Chemically treated	Chicken lencocytos	Sequence encoding		DNA encoding Leuco

## ALIGNMENTS

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RESULT 1
AAD37916
Tanapox virus (TPV) gp38 DNA.
                                                                             10-SEP-2002 (first entry)
                                                                                     AAD37916;
                                                                                          AAD37916 standard; DNA; 1034 BP.
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Immunomodulatory disorder; gp38; cancer; inflammation; allergic reaction; tumour; transplant rejection; restenosis; autoimmune complication; AIDS; acquired immune deficiency syndrome; antibody complex mediated disease; psoriasis; Behcet's syndrome; acute respiratory distress syndrome; ARDS; ischaemic heart disease; atherosclerosis; leukaemia; Addisease; type I insulin-dependent diabetes mellitus; atherosclerosis; cytostatic; gene therapy; antibacterial; cardiant; vasotropic; virucide; TPV; Tanapox virus; gene; ds.

# Tanapox virus

WO200231115-A2.		Key CDS	
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18-APR-2002.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2000; 2000US-239354P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptides, gp38 and nucleic acid molecules encoding such proteins. Sequences of the invention are useful for treating immunomodulatory disorders such as cancers, tumours, inflammation, allergic reactions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel Yatapoxvirus immunomodulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Fig 4; 75pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Yatapoxvirus immunomodulatory polypeptide, gp38, useful for treating immunomodulatory disorders, e.g. cancer, transplant rejection, asthma, ischemic heart disease, atherosclerosis, or systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1034 BP; 393 A; 147 C; 208 G; 286 T; 0 other;
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                                        TGTAAAAAACACTCTTTGGAAAGATGTAAAAACTTATCTAGGCGGTTTTTGAATACATGGG
                                                                                                AGGAGATAAAAGGTTTACGAAAATGACACATAAAGGTTTTCCCCAAGGTTGGAATGTTAAC
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Essani K;

2000US-239354P. 2001WO-US32136

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Immunomodulatory disorder; gp38; cancer; inflammation; allergic reaction; tumour; transplant rejection; restenosis; autoimmune complication; AIDS; acquired immune deficiency syndrome; antibody complex mediated disease; psoriasis; Behcet's syndrome; acute respiratory distress syndrome; ARDS; ischaemic heart disease; atherosclerosis; leukaemia; Addison's disease; type I insulin-dependent diabetes mellitus; atherosclerosis; cytostatic; gene therapy; antibacterial; cardiant; vasotropic; virucide; YLDV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yaba-like disease virus (YLDV) gp38 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTATACGACCACCTATATAGAAAAACAGAAGAAGGAGAAGGTGAAGAGGATGAAGAAGA 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                          Location/Qualifiers
                                                /product= "YLDV gp38 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel Yatapoxvirus immunomodulatory peptides, gp38 and nucleic acid molecules encoding such proteins. Sequences of the invention are useful for treating immunomodulatory disorders such as cancers, tumours, inflammation, allergic reactions, transplant rejection, restenosis, antibody complex mediated diseases, autoimmune complications of AIDS (acquired immune deficiency syndrome), psoriasis, Behcet's syndrome, acute respiratory distress syndrome (ARDS), ischaemic heart disease, type I insulin-dependent diabetes mellitus, Addison's disease, atheroselerosis or leukemia. They are also used in gene therapy. The present sequence is Yaba-like disease virus (YLDV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1017 BP; 383 A; 139 C; 207 G; 288 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Fig 6; 75pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Yatapoxvirus immunomodulatory polypeptide, gp38, useful for treating immunomodulatory disorders, e.g. cancer, transplant rejection, asthma, ischemic heart disease, atherosclerosis, or systemic lupus
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                   ACAGTGAAAGTAACGGGTAATGAGTTAGAAGATGGTAACATGACTCTTGAATGCAGTGTA
                                                                                    TTAGCTATTTTAGATTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGATACAACACCT
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ACAGTGAAAGTAACGGGTAATGAGTTAGAAGATGGTAACATGACTCTTGAATGCACTGTA
                                                                                                                                AACACTCTTTGGAAAGATGTAAAAGCTTATTTAGGCGGTTTTGAATATATGGGATGTTCA
                                                                                                                                                      AACACTCTTTGGAAAGATGTAAAAACTTATCTAGGCGGTTTTGAATACATGGGATGTTCA
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                                                                                                                                                                                                                                                                                                                                                         AGCACAAAACTACTTCGCTTTCATTAATCACTGGGTGTTATGAAACAGGATTATTATTT 367
                                                                  TTAGCTATTTTAGATTACCAAAAAATGGCTAAAAGGTAAAATACCAAAAGATACAACACCT
                                                                                                                                                                                                    AAAAGGTTTACGAAAATGACACATAAAGGTTTTCCCCAAGGTTGGAATGTTAACTGTAAAA
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                                                                                                                                                                                                                                                                                                                                         AGCACAAAAACTACTTCGCTTTCATTAATCACTGGGTGTTATGAAACAGGATTATTATTT
                                                                                                                                                                                                                                                                                                                                                                                                           AACTTTAACTTTTGGTATTCTTTAATGAAAGAAACTTTTAGAAGAAATTAATAAAAACGAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATAATTATACTGTTACGTTAAAAGATGATGGGTTATACGATGGAGTATTTTACGATCAT
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Pred. No. 8.9e-216;
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         asthma,
            New Yatapoxvirus immunomodulatory polypeptide, gp38, useful for treating immunomodulatory disorders, e.g. cancer, transplant re-
                                                                P-PSDB;
                                                                            WPI; 2002-452345/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunomodulatory disorder; gp38; cancer; inflammation; allergic reaction; tumour; transplant rejection; restenosis; autoimmune complication; AIDS; acquired immune deficiency syndrome; antibody complex mediated disease; psoriasis; Behcet's syndrome; acute respiratory distress syndrome; ARDS; ischaemic heart disease; atherosclerosis; leukaemia; Addison's disease; type I insulin-dependent diabetes mellitus; atherosclerosis; cytostatic; gene therapy; antibacterial; cardiant; vasotropic; virucide; YMTV;
                                                                                                                                   (VIRO-) VIRON THERAPEUTICS INC
                                                                                                                                                                  11-OCT-2000;
                                                                                                                                                                                          11-OCT-2001; 2001WO-US32136.
                                                                                                                                                                                                                                                       WO200231115-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yaba monkey tumor virus (YMTV) gp38 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                  monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                            monkey tumor virus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908 CATGACACTTTAGAAGCGCAAGTTTATACTTGTTCTGAAGGATGCAATGGAGAGGTATAC
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    ischemic heart disease,
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                                                                                                       Essani
                                                                                                                                                                                                                                                                                                                                                                                                                   tumor virus
                                                                                                                                                               2000US-239354P
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                                                                                                                                                                                                                                                                                       /product= "YMTV gp38 partial protein"
/transl_except= (pos:166..168, aa:Lys)
/transl_except= (pos:169..171, aa:Arg)
/note= "CDS does not include stop codon"
                                                                                                                                                                                                                                                                                 /partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptides, gp38 and nucleic acid molecules encoding such proteins. Sequences of the invention are useful for treating immunomodulatory disorders such as cancers, tumours, inflammation, allergic reactions,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Page 71; 75pp; English.
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                                                                                                                                                                                                                                                                                                     ACCGTTCATGGTCCTAGTTGGCAAACAGTTAAAAAATACGTGGGAGGGTTTGTGTACGCT
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                                                                                                                                                                                                                                                                                                                                            ACTGTAAAAAAACACTCTTTGGAAAGATGTAAAAACTTATCTAGGCGGTTTTGAATACATG 538
                                                                                                                                                                                                                                                                                                                                                                                ACGAAAGATAAAAAGTTTTTAAAAATGACAGATAAAAGGATTTCCAAAGGTTGGAATGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACCACTTTAACTTTTGGTACCCGTTAATGAAAGATACTTTGGAGTCCATCAATAGTAAT
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TTTAACGGTGAATATAGATACGTTAATGGAAGAGAATACCCGGAATGGGGAAGGCAATCA
                                   TTTAAAGGTGAATATAAATATGTTAACGGAAGATACTATCCAGAATGGGGGAGAAAATCC 778
                                                                         TGTAACGTAAAATCTTTTTACCCTCCAGACGTAATGATCAAGTGGATAGAAAGTAAATAT
                                                                                               TGCAGTGTAAATTCATTTTACCCTCCTGACGTAATTACTAAGTGGATAGAAAGCGAACAT 718
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74.5%;
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Pred. No. 4.7e-121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-2002
                                                                                                                                                                                                              New Yatapoxvirus immunomodulatory polypeptide, gp38, useful for treating immunomodulatory disorders, e.g. cancer, transplant rejection, asthma, ischemic heart disease, atherosclerosis, or systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                          McFadden G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (VIRO-) VIRON THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2000; 2000US-239354P.
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                                                                                                                                 English
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The present invention relates to novel Yatapoxvirus immunomodulatory peptides, gp38 and nucleic acid molecules encoding such proteins. Sequences of the invention are useful for treating immunomodulatory

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Query Match
Best Local S
Matches 451
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                   TACGTACAACATCAAAAATGAGTAGGTCAACTATGTGTTGTTTTTCCATGACACTTTAG 920
                                                                                  GTTTTCCATGGAATATTAAAAAAAGATAAAGATGCAAACACATATAGTTT.AACAGATTTAG
                                                                                                                                                                                          CTCCTGACGTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAGGTGAATATAAATATG 740
                                                                                                                                                                                                                                                                                                   ATTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGATACAACACCTACAGTGAAAGTAA 620
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    TTATGGTACCAACTATCATGTCTAATAGAATAGCATGTGTTTGGATTTCATAGTACGTTAG
                                                        TTAACGGAAGATACTATCCAGAATGGGGGAGAAAATCCGATTATGAGCCAGGAGAGCCAG
                                                                                                                                                                 CGTCGTCGGTCGCTGTTAAATGGTATAACATCGAGGACTTTGCTCCGGACTATCGTTATG
                                                                                                                                                                                                                      CAGGAATTGAAAGAGGAGA---TAATACTACATTGATATGCACATTTGATAATCATTATC
                                                                                                                                                                                                                                                CGGGTAATGAGTTAGAAGATGGTAACATGACTCTTGAATGCAGTGTAAATTCATTTTACC
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49.0%;
                                                                                                            -TACGTAAATGAATTGCTTCCTGATACGGACTATCTACCGGGTGAACCAG
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01-JUL-1992;
21-APR-1989;
29-JUN-1992;
14-SEP-1994;
                                  inserted into, or replacing all or a portion, of a SPV gene or nucleic acid sequence. The replaced gene or nucleic acid sequence is not essential to replication of the virus in a host cell, and is selected from a gene or nucleic acid sequence present in the HindIII C fragment. The vector can be used for the expression of heterologous proteins, both in vivo as a vaccine, and in vitro for production of the selected protein. The heterologous protein is proferrably pseudorables virus gp50 or gp63 for use in swine vaccines. As SPV is host-restricted to swine, the use of modified recombinant SPV as a live vaccine vector eliminates the risk of
                                                                                                                                                         This double-stranded DNA sequence, both strands of which are claimed, comprises the HindIII C fragment of swinepox virus (SPV). The sense strand includes putative coding regions for 6 polypeptides (AAW26408-13) and the antisense strand includes putative coding regions for 21 polypeptides (AAW26414-34). A claimed recombinant vector comprises a heterologous not expense expenses that the comprises a heterologous not polypeptide sequence
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94US-0307499.
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89US-0342212.
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                                                                               TACGTACAACATCAAAAATGAGTAGTCAACTAGTATGTGTTTTTCCCATGACACTTTTAG
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AACCAAGCATATATAGATGT
                             AAGCGCAAGTTTATACTTGT
                                                                                                                          GTTTTCCATGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGATTTAG
                                                                                                                                                                                      ATCCG-----TACGTAAATGAATTGCTTCCTGATACGGACTATCTACCGGGTGAACCAG
                                                                                                                                                                                                                     TTAACGGAAGATACTATCCAGAATGGGGGAGAAAATCCGATTATGAGCCAGGAGAGCCAG
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RESULT 6
AAF84948/C
ID AAF849

AAF84948 standard;

DNA; 14176

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Query Match
Best Local Similarity
                                                      The present sequence represents a HindIII C fragment of Swinepox virus (SPV). The polynucleotide fragment was used to construct a recombinant vector. The vector comprises a heterologous nucleotide sequence encoding a protein from a selected pathogen inserted into, or replacing, all or a portion of a swinepox virus gene, which is not essential to replication of the virus in a host cell. The SPV vector is useful in diagnostic, therapeutic or prophylactic compositions. In particular, the vector is useful as a vaccine or a therapy against a selected pathogen, particularly against pseudorables. The vector is also useful in therapeutic or vaccine compositions against TGEV (undefined), African swine fever virus, porcine parvovirus, swine influenza, hoy cholera or other bacterial mathogen.
                                                                                                                                                                                                                                                                                                                           14-SEP-1994;
21-APR-1989;
02-JUL-1992;
28-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPV;
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                                                                                                                                                                             Claim
                                                                                                                                                                                                      New recombinant swine poxvirus vector, useful in diagnostic, therapeutic or prophylactic compositions, e.g. as a vaccine against therapeutic fever virus, porcine parvovirus, swine influenza, or
                                                                                                                                                                                                                                                                                                                                                                           26-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                             17-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Swinepox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the HindIII C fragment of Swinepox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-2001
                              Sequence 14176 BP;
                                                                                                                                                                                                                                                P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector; pathogen;
                                                bacterial pathogens.
                                                                                                                                                                           8; Fig 2; 116pp; English.
                                                                                                                                                                                                                                                                             RW,
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                                                                                                                                                                                              against pseudorabies
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89US-0342212.

92US-0908241.

97US-0901127.

92US-0908630.
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                             4820 A; 2231 C; 1639 G;
  12.9%;
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  Score 133
Pred. No.
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 133.6; DB 2
No. 7.2e-21;
                             5486 T; 0 other;
          22;
                                                    (undefined), Array
how cholera
         Length 14176;
RESULT 7
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TTAATATTTCTAGGAGTCCCCACACGCCAGGTAACGATTACAACTTTAACTTTTGGTATT
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                                  AAGCGCAAGTTTATACTTGT
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12829.
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                    "encodes AAB68252"
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21-APR-1989;
02-JUL-1992;
28-JUL-1997;
29-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the reverse complement of a HindIII C fragment of Swinepox virus (SPV). The polynucleotide fragment was used to construct a recombinant vector. The vector comprises a heterologous nucleotide sequence encoding a protein from a selected pathogen inserted into, or replacing, all or a portion of a swinepox virus gene, which is not essential to replacation of the virus in a host cell. The SPV vector is useful in diagnostic, therapeutic or prophylactic compositions. In particular, the vector is useful as a vaccine or a therapeutic or prophylactic compositions. In particular, the vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine or a therapeutic vector is useful as a vaccine vector is useful as vaccine vector is useful as a vaccine vector is useful as vaccine vector is useful a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14176 BP; 5486 A; 1639 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant swine poxvirus vector, useful in diagnostic, therapeutic or prophylactic compositions, e.g. as a vaccine against African swine fever virus, porcine parvovirus, swine influenza, or especially against pseudorables -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy against a selected pathogen, particularly against pseudorables. The vector is also useful in therapeutic or vaccine compositions agains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8;
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ATGTAGAAACGGCCAACGGACCGTTGGCCAGATACCATACAGGAGATAAAAGGTTTACGA 440
                              AGACTATGTCCTTGACAATTGGATGTACTGATCTAAGACAACTTCAAGTAAATTTCGGTT
                                                                                              ATAGAATGAGTGAAACGCTAGATGAGATAAATAAACTTCCAGAAACGAGTAATCCTTACA 13482
                                                                                                                  TTAATGAGACTAAGATTAGATATTATCCGAAAAATAATTATAATTTTATGTTCTGGCTAA
                                                                                                                                                                                              TTAATATTTCTAGGAGTCCCCACACGCCAGGTAACGATTACAACTTTAACTTTTGGTATT
                                                                                                                                                                                                                              GTTTAAAACTAAATAGCGAGACAGGAAGACCAGAATTAAGAAATGAACCACCAACATGGT
                                                                                                                                                                                                                                                          CGAAAATATCATATAACCACGAAACTAGACACGGAAACGTAAATTTTAGGGCTGATTGGT
                                                                                                                                                                                                                                                                                          ATGATAATCATCGATATGACTTCGAAGTCACCGATTATTTTAATGATATACTAATAAAAC
                                                                                                                                                                                                                                                                                                                         TAAAAGATAATGGGTTATACGATGGAGTATTTTACGATCATTACAACGATCAGTTAGTAA
                                                                                                                                                                                                                                                                                                                                                       TTACAGCATATGTAGATGCTTCCGCATTCTTAGTATACAATTATACATATACTTTACAAG 13242
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                                                     -CGCTTTCATTAATCACTGGGTGTTATGAAACAGGATTATTTTGGTAGTTATGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  also useful in therapeutic or vaccine compositions against d), African swine fever virus, porcine parvovirus, swine cholera or other bacterial pathogens.
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89US-0342212.

92US-0908241.

97US-0901127.

92US-0908630.
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Pred. No. 7.
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                                                        WO200231115-A2
                                                                                                                                                                                                 Yaba monkey tumor virus
                                                                                                                                                                                                                                                                                                                                Immunomodulatory disorder; gp38; cancer; inflammation; allergic reaction,
                                                                                                                                                                                                                                                                                                                                                                  Yaba monkey tumor virus (YMTV) gp38 partial DNA.
                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD37915 standard;
                           18-APR-2002.
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                                                                                                                                                                                                                              monkey tumor virus; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                 /*tag= a
/product= "YMTV gp38 partial protein"
/note= "CDS does not include stop codon"
                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
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Best Local :
                                                                                                Human; cytostatic; neuroprotective; nootropic; immunostimulant; gene therapy; gene regulation; DNA replication; CEMPB; DNA2L; ATR; CHD1L; ERCC3; SNRPAL; RAD50; LIG2; cytosine methylation; Ataxia telangiectasia; ATR-X; Bloom's syndrome; tumour; cancer; methylation; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel Yatapoxvirus immunomodulatory peptides, 938 and nucleic acid molecules encoding such proteins. Sequences of the invention are useful for treating immunomodulatory disorders such as cancers, tumours, inflammation, allergic reactions, transplant rejection, restenosis, antibody complex mediated diseases, autoimmune complications of AIDS (acquired immune deficiency syndrome), psoriasis, Behcet's syndrome, acute respiratory districts syndrome (ARDS), ischaemic heart disease, type I insulin-dependent diabetes mellitus, Addison's disease, atherosclerosis or leukemia. They are also used in gene therapy. The present sequence is Yaba monkey tumor virus (YMTV)
                                                                                                                                                                             Human polynucleotide associated with DNA replication
                                                                                                                                                                                                              01-MAY-2002
                                                                                                                                                                                                                                           ABL49349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Yatapoxvirus immunomodulatory polypeptide, gp38, useful for treating immunomodulatory disorders, e.g. cancer, transplant rejection, asthma, ischemic heart disease, atherosclerosis, or systemic lupus
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                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                       standard; DNA; 6306
                                                                                                                                                                                                                                                                                                                                                  GTAAAT 183
                                                                                                                                                                                                                                                                                                                                                                               GTAAAT 190
                                                                                                                                                                                                                                                                                                                                                                                                           TATTACAACGATCAGTTAGTAACGAGGATATCATATAATCATGAAACCAAACGAGGAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATATAATTATACGTTTACGTTAAAAGATAATGGGTTATACGATGGAGTATTTTACGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 98;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to nucleic acid sequences comprising at least 18 cd bases of a chemically pretreated gene associated with gene regulation, selected from 94 genes (ABIA9301-ABIA9394) and/or complementary sequences associated with DNA replication, CENPB, DNA21, ATR, CHDIL, ERCC3, SNRPA1, RAD50 and LIG2. The chemical pretreatment converts cytosine bases cummethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences and method are useful in the CC diagnosis of diseases (or predisposition to diseases) associated with DNA replication and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes. They are especially useful in diagnosis and therapy of e.g. Ataxia telangiectasia, ATR-X, Bloom's cytosine methylation patterns of such genes. They are especially useful in diagnosis and therapy of e.g. Ataxia telangiectasia, ATR-X, Bloom's cytosine methylation and cancer.

CC syndrome, solid tumours and cancer.

CC vote: The sequence data for this patent did not form part of the printed cytosine, solid tumours and cancer.

CC vote: The sequence data for this patent did not form wife of the printed cytosine produced to that referred to in the specification. The present data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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07-APR-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-)
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                                                                                   TTTTCCATGGAATATTAAAAAAAGATGAAAGATGCAAACACATATAGTTTAACAGATTTAGT
                                                                                                                                                   TTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGATACAACACCTACAGTGAAAGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGATGTAAAAACTTATCTAGGCGGTTTTGAATACATGGGATGTTCATTAGCTATTTTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from EPO data for the patent.
TAGATGACGGATTATTAAATATGAAAAGGTAAAATTTTTAAATATTTTTAGGAAAAATAGAAT
                                                                                                                                                                                                 TAACGGAAGATACTATCCAGAATGGGGGAGAAAATCCGATTATGAGCCAGGAGAGCCAGG
                                                                                                                                                                                                                                                         TTTAAGGTGATAAGTGAAGGTGGTAAAAAGGTGATATAGTTAAAATTATATTAGGATAATT
                                                                                                                                                                                                                                                                                                                                                            TGGTTTAGGGATAGAAAATAGATTTATAGAATAGAATTGATTTTATATATATTTGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                             GGGTAATGAGTTAGAAGATGGTAACATGACTCTTGAATGCAGTGTAAATTCATTTTACCC
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; 2000DE-1019173.
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Matches 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ87587-89 encode polypeptides having a whole or partial epitope of a structural protein of Leucocytozoan protozoa (see AAR70491-93). The polypeptides and DNA encoding them are useful in the production of vaccines for the treatment of leucocytozoanosis of fowl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ87587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1686 BP; 915 A; 129 C; 382 G; 260 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-167252/22.
P-PSDB; AAR70491.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immune inducing polypeptide against Leucocytozoan protozoa -
in production of vaccines for treatment of leucocytozoanosis
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(NISS-) NISSEIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leucocytozoan protozoa; structural leucocytozoanosis; treatment; ss.
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                                             886 TCAACTAGTATGTGTTTTTCCATGACACTTTAGAAGCGCAAGTTTATACTTGTTCTGA 945
                                                                                                                                                                                                                                      766 GGGGAGAAAATCCGATTATGAGCCAGGAGAGCCAGGTTTTCCATGGAATATTAAAAAAGA 825
                                                                                                                                                                                                                                                                                     706 AGAAAGCGAACATTTTAAAAGGTGAATATAAATATGTTAACGGAAGATACTATCCAGAATG 765
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                         Page 12-14; 20pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA; 1686
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TGAAGAAGAACAAATGAAGATGAACAAAATGAAGATGAACAAAATGAAGAAGAAGAAGA
                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49.4; DB 16;
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                                                                                                                    Query Match
Best Local
                                                                                                      Matches
                                                                                                                                                                                      The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                      Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL33307;
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                                                                                                                                                               Sequence
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                19
                                                                                                                    Similarity
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                                                                                                                                                                 6175
                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1280; 32pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAAGAAGAAGAAGAAGAAC
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                                                                      AAGCTTCATGAATAAGTTAATTATTTAGCACAATTGTAGCAGTTTGTAACTGCATAAC
                                                                                                     Conservative
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2000DE-1043826
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Best Local Similarity
Matches 200; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (AAN60472) or FIRA (AAN60473). RESA and F. antigenicity suitable for providing protective immunity against plasmodium falciparum malarial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 1; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ART05868 encodes a chicken leucocytozoan immunogenic protein, this Di or a fragment of it can be used in a recombinant vaccine to immunise against chicken leucocytozoan disease. The DNA is used in a vector and operatively linked to an expression regulatory sequence as in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chicken leucocytozoan immunogenic protein vaccine against chicken leucocytozoan dise
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            practice.
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           AGGTTTTCCATGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGATTT
                                                                               TGTTAACGGAAGATACTATCCAGAATGGGGGAGAAAATCCGATTATGAGCCAGGAGAGCC
                                                                                                                                                                          CCCTCCTGACGTAATTACTAAGTGGATAGAAGCGAACATTTTAAAGGTGAATATAAATA
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use as insert in a recombinant vaccine
use as insert in a recognition of the claims, ror
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                                           signalling, as well as oligonucleotides and/or pNA-oligoners for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of generic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling.

Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                     The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell
                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemically treated cell signalling DNA sequence#109
                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 217; 24pp+sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OLek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell signalling; cytosine methylation; cell signalling disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL70327 standard; DNA; 6012 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2001; 2001WO-EP07471.
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                                   Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAGTAACACATGAAGAAGAAGAAAAGTAACACATGAAGAAGAAGA 3068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGAAAAACAGAAGAAGGAGAAGGTGAAGAAGAAGAAGAAGAAGAAA 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAGAAGAAATGTAACATATGAAGAAGAAGAAGAAAAAGTAACACATGAAGAAGAAGA 3020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAAGCGCAAGTTTATACTTGTTCTGAAGGATGCAATGGAGAGCTATACGACCACCTATA 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACACATGAAGAAGAAGAAAAAAGTAACACATGAAGAAGAAGAAAAAGTAACACATGA 2960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTACGTACAACATCAAAAATGAGTAGTCAACTAGTATGTGTTGTTTTCCATGACACTTT 918
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414 ACCATACAGGAGATAAAAGGTTTACGAAAATGACACATAAAGGTTTTCCCAAGGTTGGAA

Matches 110; Query Match Best Local

Similarity

4.5%;

Score 47; Pred. No.

0 B .35;

24; Length 6012;

Conservative

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Mismatches

105;

Indels

0;

Gaps

Sequence 6012 BP; 1785 A; 32 C; 958 G;

3237

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0 other;

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Is bases of a chemically pretreated gene associated with gene regulal selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardia disorders, haemophilia, solid tumours and cancer, Werner syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; precelampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                           The
                                                                                                                                                                                                                                                                             Disclosure; SEQ ID No 235; 26pp; English.
                                                                                                                                                                                                                                                                                                                                   New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2001; 2001WO-EP03968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene regulation-associated gene oligonucleotide #229
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-017470/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nephrotropic; gynecological; anti-tumour; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-)
                                                                                                                                                                                                               invention relates to 224 nucleic acid sequences comprising at least bases of a chemically pretreated gene associated with gene regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA; 6012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAACTAAAAACACCACTTTATAAAAAAATTTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTTAACTGTAAAAAACACTCTTTGGAAAGATGTAAAAACTTATCTAGGCGGTTTTGAAT 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGATACAACACCTACAGTGAAAGTAACGGGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                 genes,
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                                                                                                                                                                                                                                                                                                                       Query Match 4.5%; Score 47; DB 24; Length 6012; Best Local Similarity 51.2%; Pred. No. 0.35; Matches 110; Conservative 0; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preeclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6012 BP; 1785 A; 32 C; 958 G; 3237 T; 0 other;
                                                                              4536 TAACTAAAAACACCACTTTATAAAAAAATTTCAT 4502
                                                                                                       534 ACATGGGATGTTCATTAGCTATTTTAGATTACCAAAAAATGGCTAAAGGTGAAATACCAA 593
                                                                                                                                                                                 474 TGTTAACTGTAAAAACACTCTTTGGAAAGATGTAAAAACTTATCTAGGCGGTTTTGAAT 533
                                                                                                                                                                                                                                                            414 ACCATACAGGAGATAAAAGGTTTACGAAAATGACACATAAAGGTTTTCCCAAGGTTTGGAA 473
                                    594 AAGATACAACACCTACAGTGAAAGTAACGGGTAAT 628
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Search completed: June 15, 2003, 20:25:31 Job time: 296 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
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Gapop 10.0 , Gapext 1.0
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1034
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-559-896B-1

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US-08-998-416-185

US-08-998-416-786

US-08-998-416-786

US-08-998-416-538

US-08-998-416-538

US-08-998-416-538

US-08-998-416-305

US-08-998-416-305

US-08-998-416-37

US-08-998-416-37

US-08-9134-001C-1621

US-08-998-416-701

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US-08-998-416-534

US-08-998-416-534
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                                                  Sequence 53, Appl Sequence 1, Appl Sequence 1, Appl Sequence 14, Appl Sequence 19, Appl Sequence 191, Appl Sequence 191, Appl Sequence 1036, App Sequence 683, App Sequence 538, App Sequence 538, App Sequence 13, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 7, Appl Sequence 71, App Sequence 71, Appl Sequence 534, App Sequence 534, Ap
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      equence
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35	35	35.2	35.4	35.4	35.4	35.4	35.4	35.4	35.4	35.4	35.6	35.8	36	36	36	36	36.6
3.4	3.4	3.4	3.4	3.4	3.4	3.4		3.4		3.4	3.4	з 5	3.5	ω .5	3 .5	3.5	3 5
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PCT-US93-07261-10	US-08-741-134-5	US-08-929-329-3	US-09-193-931C-4	US-09-103-478-4	5196523-5	US-08-441-139-12	US-08-257-073-10	US-09-193-931C-3	US-09-103-478-3	US-09-072-596-334	US-09-797-906-3	US-08-238-163-3	US-08-915-136-27	US-08-405-496A-27	US-08-480-604A-27	US-08-998-416-595	US-09-435-377-1
Sequence 10, Appl	Sequence 5, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 4, Appli	٠	Sequence 12, Appl	Sequence 10, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 334, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 27, Appl	Sequence 27, Appl	Sequence 27, Appl	Sequence 595, App	Sequence 1, Appli

### ALIGNMENTS

RESULT 1 US-08-307-499-53

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Sequence 53, Applicati
Patent No. 5651972
GENERAL INFORMATION:
APPLICANT: Moyer,
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/307,499
ETILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILLING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILLING DATE: 29-JUN-1992
                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as
TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
COMBERR OF SEQUENCES: 60
                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION: 435
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 2421
CITY: Gainesville
                                                                                                   TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
TYPE: nuclei
STRANDEDNESS:
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                                     LENGTH:
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                   nucleic acid
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                                     1023 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
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; TOPOLOGY: un ; MOLECULE TYPE: US-08-307-499-53

unknown

DNA (genomic)

Matches 451; Conservative

35

Local Similarity

12.9%;

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Mismatches

Query Match Best Local :

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ATGTAGAAACGGCCAACGGACCGTTGGCCAGATACCATACAGGAGATAAAAGGTTTACGA 440
                                                                                                                                      TACGTACAACATCAAAAATGAGTAGTCAACTAGTATGTGTTTTTCCATGACACTTTAG
                                                                                                                                                                                  GTTTTCCATGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGATTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGATGTAAAAACTTATCTAGGCGGTTTTGAATACATGGGATGTTCATTAGCTATTTTAG
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                                                                                               TTATGGTACCAACTATCATGTCTAATAGAATAGCATGTGTTTGGATTTCATAGTACGTTAG
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Pred. No. 1.4e-25;
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                                                                                                                                                                                                                                                                          Matches 451;
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sallwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 21-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchi)
STREET: 2421 N.W. 41st Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as
TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                  Local
      155
                                                                                                                                      87
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                                                                                                                                                                                                            27 TTAGCACAATTGTAGCAGTTTGTAACTGCATAACTTTAAAATATAATTATACTGTTACGT
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Similarity 49.0%;
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                                                                                                                                 TAAAAGATAATGGGTTATACGATGGAGTATTTTACGATCATTACAACGATCAGTTAGTAA 146
GTTTAAAACTAAATAGCGAGACAGGAAGACCAGAATTAAGAAATGAACCACCAACATGGT
                                         CGAAAATATCATATAACCACGAAACTAGACACGGAAACGTAAATTTTAGGGCTGATTGGT
                                                                                     ATGATAATCATCGATATGACTTCGAAGTCACCGATTATTTTAATGATATACTAATAAAAC
                                                                                                                                                                           TTACAGCATATGTAGATGCTTCCGCATTCTTAGTATACAATTATACATATACTTTACAAG
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                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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                                                                                                                                                                                                                                                                      Score 133.6;
Pred. No. 1.4e
0; Mismatches
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                                                                                                                                                                                                                                                                                           6; DB 4;
1.4e-25;
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                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                Length 1023;
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AACCAAGCATATATAGATGT

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207 TTAATATTTCTAGGAGTCCCCACACGCCAGGTAACGATTACAACTTTAACTTTTGGTATT

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RESULT 3
US-08-307-499-1/c
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APPLICANT: Moyer, 1
APPLICANT: V1 uela
APPLICANT: Gibbs, 1
                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08307499 Patent No. 5651972
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                         ADDRESSEE: David R.
                                                                                                                                                                                                            APPLICANT: Moyer, Richard W.
APPLICANT: V1 uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as
TITLE OF INVENTION: Live Vaccine Vector
                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                 STREET: 2421 N.W. CITY: Gainesville STATE: Florida
                                                               ZIP:
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                                                                                                                                     3: David R. Saliwanchik
2421 N.W. 41st Street,
                                                                               U.S.A.
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APPLICATION NUMBER: US 07/
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 29-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 07/342,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME/KEY:
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                                                     TTAATGAGACTAAGATTAGATATTATCCGAAAAATAATTATAATTTTATGTTCTGGCTAA
                                                                                           TTAATATTTCTAGGAGTCCCCACACGCCAGGTAACGATTACAACTTTAACTTTTGGTATT
                                                                                                                                 GTTTAAAACTAAATAGCGAGACAGGAAGACCAGAATTAAGAAATGAACCACCAACATGGT
                                                                                                                                                                     CGAAAATATCATATAACCACGAAACTAGACACGGAAACGTAAATTTTAGGGCCTGATTGGT
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Pred. No. 3.4e-25;
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                                                                                                                                                                                                                                                      Patent No. 5651972
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Wi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as
TITLE OF INVENTION: Live Vaccine Vector
                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08307499 Patent No. 5651972
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: .
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
   FILING DATE:
                                                                                                                                                  COUNTRY:
                                                                                                                                                                                 CITY: Gainesville
                  APPLICATION NUMBER:
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                                                                                                                                                                  Florida
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TOPOLOGY: unki
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APPLICATION NUMBER: US 07/908,241

FILING DATE: 1-JUL-1992

PRIOR APPLICATION NUMBER: US 07/908,630

APPLICATION NUMBER: US 07/908,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David
REGISTRATION NUMBER: 31,7
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APPLICATION NUMBER: US 0
FILING DATE: 21-APR-1992
FEATURE:
NAME/KEY:
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                      14014 TTATGGTACCAACTATCATGTCTAATAGAATAGCATGTGTTGGATTTCATAGTACGTTAG 14073
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                                                             TACGTACAACATCAAAAATGAGTAGTCAACTAGTATGTGTTTTTTCCATGACACTTTAG
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Similarity 49.08;
                                                                                                          GTTTTCCATGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGATTTAG
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GENERAL INFORMATION:
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LOCATION:
FEATURE:
NAME/KEY:
                                                             FEATURE:
NAME/KEY:
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LENGTH: 14176 base pairs
TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
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APPLICATION NUMBER: US 07/342,212
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APPLICATION NUMBER: US 0:
FILING DATE: 29-JUN-1992
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MEDIIM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
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6217882
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2421 N.W. 41st Street, Suite A-1
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5131..5310
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4585..4887
CDS
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AACCAAGCATATATAGATGT 84
                                        AAGCGCAAGTTTATACTTGT 940
                                                                                                                     TACGTACAACATCAAAAATGAGTAGTCAACTAGTATGTGTTTTCCCATGACACTTTAG
                                                                                                                                                                                                  GTTTTCCATGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGATTTAG 860
                                                                                                                                                                                                                                            ATCCG-----TACGTAAATGAATTGCTTCCTGATACGGACTATCTACCGGGTGAACCAG
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RESULT 6
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Patent No. 6217882
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                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: V1 uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as
TITLE OF INVENTION: Live Vaccine Vector
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PRIOR APPLICATION NUMBER: US 07/908,630
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ADDRESSEE: David R. Saliwanchik
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US 0
FILING DATE: 21-APR-1992
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APPLICATION NUMBER:
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                                                      ATGTTACTGTAGGTGGTAATATATGGACACGATTCGACCCCAAGAATAAACGCTTTAGTA 13602
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6928..7431
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13149..14171
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11971..12780
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8715.
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8215.
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6171.
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10316..11908
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9562:.10272
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7454..7858
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6447..6875
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 Score 133.6; DB 4; Length Pred. No. 3.4e-25; 0; Mismatches 454; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 14176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FLAKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,46
                                                                                                                                                                                                                                                                                                                                                 ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
               TELEPHONE: (703)836-9300
                                                  APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                          FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1800 Diag
CITY: Alexandria
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(703)683-4109
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                                                    30472/114 IMMU
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.8%; Score 59.8; DB 1; Length 7218; Best Local Similarity 6.1%; Pred. No. 3.2e-06; Matches 25; Conservative 222; Mismatches 164; Indels 0
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SEQUENCE CHARACTERISTICS:
                                                                                                          CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Patrick E. Duffy
APPLICANT: Christian F. Ockenhouse
TITLE OF INVENTION: SEQUESTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                               MEDIUM TYPE: Floppy disk COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintos SOFTWARE: Microsoft Word
                                                                         CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                STREET: USA MRMC - MCMR-JA
CITY: FORT DETRICK, FREDERICK
STATE: MARYLAND
                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                   DATE
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                                                                                                                                                                     Macintosh 7.5
                                                                                                            US/08/559,896B
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                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
           NAME: Einhorn, Gregory P. REGISTRATION NUMBER: 38,4
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US-09-004-838-70
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 09-JAN-1998
                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Meyers, Blake TITLE OF INVENTION: Proce TITLE OF INVENTION: Confe NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                   CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Nucleic acid
CLASSIFICATION: 800
                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Moran, John REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1071 ACTITATAAAGAAGAATTAGATAGAATGGATAGAGAAGCAAGGTATGAAATCCCCATGAG 1130
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                                                                                                                                                                                            94111-3834
                                                                                                                                                                                                                                                         San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAAAAAAATAAGAAAGAAAATGTAATGTATTTATAATACACGACAATAATGATAGTAA 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGATACTATCCAGAATGGGGGAGAAAATCCGATTATGAGCCAGGAGAGCCAGGTTTTCCA 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAATTTAAGCAGAAATGAAAAGATAATATTATACATAGAAATATTAAAAATGAATCTAA 1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGTTAGAAGATGGTAACATGACTCTTGAATGCAGTGTAAATTCATTTTACCCTCCTGAC
                                                                                                                                                                                                                                   California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1956 base pairs
                                                                                                                                                                                                                                                                           Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                         Shen, Kathy
                                                                                                                                                                                                                                                                                                                                                                                                                                               Michelmore, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (301)
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                                                                                                                                                                                                                                                                                                                                                            Procedures and Materials for Conferring Pest Resistance in Plants
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                                       US/09/004,838
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US-08-998-416-191
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                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 191, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 70:
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LENGTH: 4163 base pairs
TYPE: nucleic acid
                 APPLICATION NUMBER: CH 0 FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GENOMIC DNA SEQU
TITLE OF INVENTION: AND USES THEREOF
                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                              STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina
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LOCATION: 1..4163
OTHER INFORMATION:
                                                                                                                                                                                                                                                                              COUNTRY:
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Local Similarity 40.38;
es 79; Conserva+1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 ATTTAGCACAATTGTAGCAGTTTGTAACTGCATAACTTTAAAATATAATTATACTGTTAC 84
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Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACGAAAATATCATATAACCACGAAACTAGACACGGAAACGTAAATTTTAGGGCTGATTG 204
                                                                                                                                                                                                                                                                              USA
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Steiner, Sabine
Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                      Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Philippsen, Peter
                                                                                                                                                                                                                                                                                                                                                  No. 6239264artis Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rainer
                                                    CH 0016/97
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US-08-998-416-185/c
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TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
                                                                                                                                                                                                                                                                                                                                                                               Sequence 185, Application US/08998416 Patent No. 6239264
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                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: PAG
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                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                  ADDRESSEE: No. 6239264artis Co
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
                                         ZIP: 27709
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Local Similarity 45.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 TTACTAATTAATAATTAAATAATAATAAAAAAAGATTTAATTAATTTATATACTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 TTATTTGGTAGTTAT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 ATAAATATTATGAAAGGTACATTTAATAATTATATATATCAATGAAGTAAATTAAATAAT
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                                                          USA
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Steiner, Sabine
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                                                                                                                             6239264artis Corporation
                                                                                                                                                                                                                                                                                                                          Rainer
                                                                                                                                                                                                                                                                                                                                          Peter
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                                                                                                                                                                          RESULT 12
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                                                                                                                        Sequence 786, Application US/08998416 Patent No. 6239264
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                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                            APPLICANT:
APPLICANT:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE, DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/998,416
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                                APPLICANT:
                                                APPLICANT:
                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 24-DEC-1997
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                                                                                                                                                                                                                    242 AT 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 TAATATTATTTAGCACAATTGTAGCAGTTTGTAACTGCATAACTTTAAAATATAATTATA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                            AAACTACTTCGCTTTCATTAATCACTGGGTGTTATGAAACAGGATTATTATTTGGTAGTT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTTAGTAACGAAAATATCATATAACCACGAAACTAGACACGGAAACGTAAATTTTAGGG 197
                                                                                                                                                                                                                                                   AT 376
                                                                                                                                                                                                                                                                                TTAATATTAAAATTAAATTAAATACTATTTAATAAATATTCTATAAGTAATTTCTTATTT
                                                                                                                                                                                                                                                                                                                                           ACTTTTGGTATTCTTTAATGAAAGAAACTTTAGAAGAAATTAATAAAAACGATAGCACAA 314
                                                                                                                                                                                                                                                                                                                                                                                                        AAGGTACATTTAATAATTATATATATCAATGAAGTAAATTAAATAATTTATATAAATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGATTGGTTTAATATTTCTAGGAGTCCCCACACGCCAGGTAACGAT---TACAACTTTA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTAAAGGGTAGACTATTAAATAGAAATATTACTAGACTAATAAAAATAATATTATGA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTTACGTTAAAAGATAATGGGTTATACGATGGAGTATTTTACGATCATTACAACGATC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            662 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               919-541-8689
            Wendland, Jurgen
Knechtle, Philipp
                                           Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM:
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                                                                                            Philippsen,
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31-DEC-1996
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                                                                            Rainer
                                                                                            Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241 REFERENCE/DOCKET NUMBER: PF. TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
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MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 711 base pairs
TYPE: nucleic acid
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 919-541-859
TELEFAX: 919-541-8689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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256 TAATTTCTTATTTAT 242
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                                                                                                                                                                                                                                                                                                                 125 CATTACAACGATCAGTTAGTAACGAAAATATCATATAACCACGAAACTAGACACGGAAAC
                                                                                                                                                                                                                                                                                                                                                    556 GATAATAAATTATTAGATTTAAGTATTCTTAATAATATATTATTAGGTAAATATTTAGTA 497
                                                                                                                                                                                                                                                                                                                                                                                                                        616 TTACTAATTAATAATTAAATTAAATAATAAAAAAAAGATTTAATTAATTTATATACTTTA
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                                                                                                                                                                                                                                                                                                                                                                                     65 AAATATAATTATACTGTTACGTTAAAAGATAATGGGTTATACGATGGAGTATTTTACGAT
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Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                               TTATTTGGTAGTTAT 376
                                                                    AACGATAGCACAAAAACTACTTCGCTTTCATTAATCACTGGGTGTTATGAAACAGGATTA 361
                                                                                                                                        ---TACAACTTTAACTTTTGGTATTCTTTAATGAAAGAAACTTTAGAAGAAATTAATAAA 301
                                                                                                                                                                                                              ATAAATATTATGAAAGGTACATTTAATAATTATATATATCAATGAAGTAAATTAAATAAT
                                                                                                                                                                                                                                             GTAAATTTTAGGGCTGATTGGTTTAATATTTCTAGGAGTCCCCACACGCCAGGTAACGAT
                                                                                                                                                                                                                                                                                GGTAGTAATATCCAATTAAAGGGTAGACTATTAAATAGAAATATTACTAGACTAATAAAA
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illarity 45.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Pred. No. 0.34;
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US-08-998-416-683/c
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
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TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meigs, J. Timo
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
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                                                                                                                                                                                                                                                                                                                                              Local Similarity
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Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 724 base pairs nucleic acid
---TACAACTTTAACTTTTGGTATTCTTTAATGAAAGAAACTTTAGAAGAAATTAATAAA 301
                                   GTAAATTTTAGGGCTGATTGGTTTAATATTTCTAGGAGTCCCCACACGCCAGGTAACGAT 244
                                                                                                        GGTAGTAATATCCAATTAAAGGGTAGACTATTAAATAGAAATATTACTAGACTAATAAAA 436
                                                                                                                                                                            GATAATAAATTATTAGATTTAAGTATTCTTAATAATATATTATTAGGTALATATTTAGTA 496
                                                                                                                                                                                                                                                   TTACTAATTAATAATTTAAATAATAATAATAAAAAAAGATTTAATTAATTTATATATTTA 556
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Knechtle, Philipp
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Steiner, Sabine
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Pred. No. 0.34;
0; Mismatches
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                                                                                                     Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: PAG
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 732 base pairs
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APPLICATION NUMBER: CH 0
FILING DATE: 31-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
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65 AAATATAATTATACTGTTACGTTAAAAGATAATGGGTTATACGATGGAGTATTTTACGAT 124
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Research Triangle Park: No. 6239264th Carolina
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Steiner, Sabine
Mohr, Christine
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/ENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
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Knechtle, Philipp
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.34;
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APPLICANT:
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PRIOR APPLICATION DATE: CH 0016/97
APPLICATION (NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
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                                                                                                            SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                  NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241
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CITY: Research Triangle Park
STATE: No. 6239264th Carolina
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VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
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Knechtle, Philipp
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Pred. No. 0.36;
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AL147405 Anopheles
AZ548467 ENTEK30TR AL075432 Drosophil AL060767 Drosophil AU053236 AU053236 AL071865 Drosophil AL069706 Drosophil BJ422197 BJ422197 AL071865 Drosophil AL104456 Drosophil AL058896 Drosophil AL285149 Tetraodon AL175696 Tetraodon AL106647 Drosophil AL051882 Drosophil AL1099163 AL101327 AL063921 AL060100 Drosophil AL069493 Drosophil BM545225 AGENCOURT AZ551092 ENTFJ22TF AL060100 Drosophil AL062049 Drosophil AL098433 Drosophil AL069440 Drosophil AL168128 Tetraodon BQ596570 PfESToabl AL06393 AL063008 B Drosophil
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ALIGNMENTS

RESULT 1 BE421968

LOCUS

DEFINITION BE421968 1161 bp mRNA linear EST 24-JUL HWM017cF.08r ITEC HWM Barley Leaf Library Hordeum vulgare cDNA clone HWM017cF.08, mRNA sequence. BE421968 EST 24-JUL-2000

ACCESSION BE421968.1 GI:9419811

VERSION KEYWORDS

SOURCE ORGANISM Hordeum vulgare.

Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooldea;
Triticeae; Hordeum.

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REFERENCE AUTHORS TITLE

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BE421968 HWM017cF.
AL063921 Drosophil
AL064091 Drosophil
AL108811 Drosophil
AL065906 Drosophil
AL059666 Drosophil

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Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.

International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)
Contact: Wenzel G.
TU Munchen, Lehrstuhl fur Pflanzenbau und Pflanzenzuchtung Am Hochanger 2, D-85350 Freising-Weihenstephan GERMANY
Fax: 49 08161 71 5173 Email: wenzel@mm.pbz.agrar.tu-muenchen.de
International Triticeae EST Cooperative () Cooperative (ITEC)

COMMENT

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                                                                            CNS0039G 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                 CNS0039G
                          AL063921.1 GI:4941778
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/clone="HWM017cF.08"
/clone_lib="ITEC HWM Barley Leaf Library"
/tissue_type="leaf"
/dev_stage="14 day old"
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Determination of this BAC-end sequence was carried out as part
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Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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TTAACGGAAGATACTATCCAGAATGGGGGAGAAAATCCGATTA-TGAGCCAGGAGAGCCA
                                                                        CTCCTGACGTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAGGTGAATATAAATATG
                                                                                                            TAGRKWRRTWKRRWKRRDTRWDDADADDTARDDRRRRGDDGADAGKGKKTGRKRRRRDRA
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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AAAAACGATAGCACAAAAACTACTTCGCTTTCATTAATCACTGGGTGTTATGAAACAGGA 358
                                                                                     GTACGTACAACATCAAAAATGAGTAGTCAACTAGTATGTGTTTTTCCATGACACTTTA 919
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                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR08K08"
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/note="end : TET3"
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39.1%;
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                                                                                                                                                                                                 Score 59.8;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                  149 others
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Best Local
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                                                                                                                                                                                                                                                                                - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
           90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS0182P 1101 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                          PBeloBAC11
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                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTAAAGGTGAATATAAATAT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAGGAGATAAAAGGTTTACGAAAATGACACATAAAGGTTTTCCCAAGGTTGGAATGTTA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAACACCTACAGTGAAAGTAACGGGTAATGAGTTAGAAGATGGTAACATGACTCTTGAA 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- AATWIMATTAAAWATTNTAWAATAAAAAWAAAAAAAATAATAATAAAAAATAATWTATWTWAT
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     Conservative
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                                                                                              /plasmid~"pBeloBAC11"
/note="end : SP6"
268 c 128 g
                                                                                                                                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                        /clone_lib="DrosBAC"
                                                                                                                                                                             /clone="BACN37D10"
                                                                                                                                                                                                                                                   Location/Qualifiers
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                     5.6%; Score 57.4; DB 17; 19.3%; Pred. No. 0.071;
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       Mismatches
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                                                                                                                        source
                                                                                                                                                                     Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Razutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library. Or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 938)
                      /organism="Drosophila
/db_xref="taxon:7227"
/clone="BACR14J11"
/clone_lib="RPCI-98"
                                                                                                                                                  Location/Qualifiers
                                                                                       melanogaster"
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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     816 KAWKADADKDAAAKDDKADKDADKKKAKAKDDKDAKDAADADDDKAKKKDADAAKADDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             627 ATGAGTTAGAAGATGGTAACATGACTCTTGAATGCAGTGTAAATTCATTTTACCCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          867 CAACATCAAAAATGAGTAGTCAACTAGTATGTGTTTTTCCATGACACTTTAGAAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             696 KDKWWAADDKDKAAKRAAAAWAWAAADADDAKARTAKDAKAKAAKDKKKDAAKAAKDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      516 AAAAANANNANNANNNAANANNNANNNANNANAAAA 477
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                  collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Nr. The library is named Reci-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR26H19 of RPCI-98 library from Drosophila melanogaster (fruit

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as part of a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
P1 and EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAARAGAKDKDRKDAGTAATKAAAAAAKAKKKAKDDTTDTKTWDATATDKKTDGWTKKDK 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGATTTAGTACGTA 866
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                                                                                                                                                                                                                                                                                                                                    191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns
                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 843)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
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libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.4%;
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survey sequence TET3 end of BAC #
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                                                                                                                                                             Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                 Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence SP6 end of BAC BACN15C18 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL106171.1 GI:5620504 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fly), genomic survey sequence.
AL106171
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                                                                                                                                                      PBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAATAAAAWWWAATWWATWATTWAAAMAAABAATAYWAWSAAWWAWATAHAWCA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACTTTAACTTTTGGTATTCTTTAATGAAAGAAACTTTAGAAGAAATTAATAAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAAWWWAAAAAATWATATAAAAAWWWATAMAHTWTTATMAAATWWAWAATAATAHWAA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACAACGATCAGTTAGTAACGAAAATATCATATAACCACGAAACTAGACACGGAAACGTA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATWATTTWTTTATTTTAWTWTTTTTWWTATTATTAATTTWTATATWTWTATATWT 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATTTTAGGGCTGATTGGTTTAATATTTCTAGGAGTCCCCACACGCCAGGTAACGATTAC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTATWTTWATAWTTWWTAWTAAWAWTATTAWAATAWTATAWAATTAJAWTTTTWTRTA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATAATTATACTGTTACGTTAAAAGATAATGGGTTATACGATGGAGTATTTTACGATCAT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAATAAGTTAATTATTTAGCACAATTGTAGCAGTTTGTAACTGCAGAACTTTAAAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 1225)
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/db_xref="taxon:7227"
/clone="Back26H19"
/clone_lib="RRC1-98"
/note="end : TET3"
a 102 c 259 g 141 t 210
/plasmid="pBeloBAC11"
                                         /db_xref="taxon:72:
/clone="BACN15C18"
                                                               /organism="Drosophila
/db_xref="taxon:7227"
                                                                                                                             Location/Qualifiers
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                      /clone_lib="DrosBAC"
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                                                                                    melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AAACGTAAATTTTAGGGCTGATTGGTTTAATATTTCTAGGAGTCCCCACACGCCAGGTAA
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                                                                                                                                                                                                                                           Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Razutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGCTTCATGAATAAGTTAATATTATTTAGCACAATTGTAGCAGTTTGTAACTGCATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR37D06 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                           and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                          ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNSCOTTT
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR37D06"
                                                                                      Location/Qualifiers
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BACR12K22 of RPCI-98 library from
fly), genomic survey sequence.

    Web : www.genoscope.cns.fr)
    Determination of this BAC-end sequence was collaboration with the Berkeley Drosophila
    The BDGP is constructing a physical map of

                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                        CNS005TE
                                                               Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                Direct Submission
                                                                                                                  Genoscope.
                                                                                                                                            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                           Drosophila melanogaster.
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/note="end : TET3"
59 c 13 g
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Pred. No. 0.
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survey sequence TET3 end of BAC #
rom Drosophila melanogaster (fruit
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                (BDGP).
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                 EST
                              AU053236
AU053236.1 GI:4701719
                                                                                AU053236 Dictyostelium discoideum SL (H.Urushihara)
Dictyostelium discoideum
                                                                discoideum cDNA
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/note="end : TET3"
99 c 13 g
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/db_xref="taxon:7227"
/clone="BACR12K22"
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19.5%; Pred. No. 0.91
tive 157; Mismatches
                                                                clone SLI202,
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REFERENCE

(bases 1 to 538)

AUTHORS

Morio, T., Urushihara, H., Saito, Yoshino, R., Mitra, B.N., Pi, M.,

Saito, T.,

,T., Ugawa,Y., Sato,T., Taken

Takemoto, K.,

Yasukawa, H.,

Yoshida

Mizuno, H.,

ORGANISM

Dictyostelium discoideum

Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium

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RESULT 11
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SOURCE
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TITLE
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    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was collaboration with the Berkeley Drosophila

                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                GSS.
                                                                                                                                                                                                                                                                                                                                       CNS00DKY 928 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-1-1 Tennoudai, Tsu
Tel: 81-298-53-4664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Contact: Hideko Urushihara
                                                          Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                        Genoscope.
                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                   AL071865.1 GI:4948170
                                                                                                                                                                                                                                                                                                   fly), genomic survey sequence. AL071865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Tsukuba
                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGGATGAAGAAGACGGA 1024
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T = Dictyostelium discoideum cDNA
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/clone_lib="Dityostelium discoideum SL (H.Urushihara)"
/dev_stage="slug"
57 c 123 g 101 t
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/db_xref="taxon:44689"
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47.6%;
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carried out as part of a Genome Project (BDGP).
                                                            segref@genoscope.cns.fr
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VERSION KEYWORDS

GSS.

AL069706.1 GI:4949849

genomic survey sequence.

ORGANISM

Drosophila melanogaster.
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

ACCESSION

REFERENCE

AUTHORS TITLE

Genoscope

Submission

(bases 1 to 1101)

CNS00EVL

DEFINITION

CNSOOEVL 1101 bp DNA linear GSS 04-JUN-19 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit

GSS 04-JUN-1999

RESULT

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  878
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                                            372 GTTATGGGTATGT 384
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                                                                                                                                                                             119;
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/db_xref="taxon:7227"
/clone="BACR27A24"
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/note="end : T7"
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AL168128
                                                               Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 197M17 of library G from Tetraodon nigroviridis, genomic survey sequence.
           AL168128.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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/db_xref="taxon:7227"
/clone="BACR29B23"
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Human gene number estimate provided by approximation of the control of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is a single read and was generated as part of a lascale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                      AGAAAATCCGATTATGAGCCAGGAGAGCCAGGTTTTCCATGGAATATTAAAAAAAGATAAA
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/db_xref="taxon:99883"
/clone="197M17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Pred. No. 1.3;
6; Mismatches 275;
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                                                                                                                                                                Matches 154;
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                                                                                                                                                                                  Local Similarity
                                                                                     553 TATTTIAGATTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGATACAACACCTACAGT 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  553 AAAATA 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I., Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A., Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D., Waterston,R., Wilson,R. and Sibley,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU Plasmodium EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: L. David Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malaria parasite P. falciparum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang, K., Cole, R., Chakrabarti, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            falciparum cDNA 5', mRNA sequence.
BQ596570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ596570.1 GI:21543296
                                        TAATATAGATCAACAAGTAAAGGATCAAGAAAAAGTACCACAACCTTGTAGTGATGATGA 109
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                                                                                                                                                                                                                                                                                     211
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                           erythrocytes by the acidic granidalium-phenol chloroform method. The poly A+ RNA was isolated by the polyAT-Tract mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional cDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and xhoI sites of 1 2mpII vector using the Zap CDNA synthesis kit (Stragene, CA). The average size of the Clones were mass excised using the Exhasist helper phage (Strategene), the phagemids were preciptated with PEG 8000 and extracted with phenol/chloroform. Fhagemid DNA was electroporated into DHIOB cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/lab_host="pH10B (GeneHog, Invitrogen, Inc.)"
/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-lysed P. falciparum 3D7 infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:5833"
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Pred. No. 1.6;
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                                                                                                                                                                                                  DB 14;
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                                                                                                                                                Gaps
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TITLE
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549 AAAWATATKAAATTTTTTRRRTRRAGTATTTRDTRAKAAAAAAAAAAATATTAGAAAARG 608
                                                478 AACTGTAAAAACACTCTTTGGAAAGATGTAAAAACTTATCTAGGCGGTTTTGAATACAT 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  793 AGAGCCAGGTTTTCCATGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAAC 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          673 ATTTTACCCTCCTGACGTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAGGTGAATA 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP 191 94000 EVALUATION DETERMINED:

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila for anome using these BACs. For further information
                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                             Conservative 148;
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                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                   /clone="BACR01M22"
                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                     4.98;
25.98;
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                                                                                                                                                                                                                                  TET3"
148 g
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Pred. No. 1.
                                                                                                        Mismatches
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survey sequence TET3 end of BAC #
                                                                                                                                  1.8;
                                                                                                                                                        DB 17; Length 1101;
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                                                                                                                                                                                                                                     281 others
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> 2: Gaps

	AADDW 1093	1089	DЬ
	GAAGA 1020	1016	Qγ
1088	DKAKKGKAWKTTTRTDRAAKAKAKDDTAATRTATAWKDADDKAKARDAKAKWGADAKADR	1029	Db
1015	GGAGAGCTATACGACCACCTATATAGAAAAACAGAAGAAGGAGGAGAAGGTGAAGAGGATGAA	956	Qy
1028	AKAKGTGDWKKKAKKAKTGWKARADKDRWRAAADDTRWRTKAWWWTDWRWATATKDKDTK	969	Db
955	TGTGTTGTTTTCCATGACACTTTAGAAGCGCAAGTTTATACTTGTTCTGAAGGATGCAAT	896	Qy
968	DKGRRAGWGTGWRRRARARTRKAKAKRRGARAGAKAKRRAKGDAWKDGWKKKWDKDAAWA	909	DЬ
895		836	Qy
908	DGTRARRARGAGDGWDAKAAWAWAAAWAATTARWDTATAADDRRAKAWDKRAAAAADRDK	849	Ъ
835	TCCGATTATGAGCCAGGAGAGCCAGGTTTTCCATGGAATATTAAAAAAGATAAAGATGCA	776	Qy
848	TAAWKKDWKATDAAAAKAAARTRDWTTAKAKDKTKWGAAAATGAWGAGAARGRRWGRKGK	789	В
775	CATTTTAAAGGTGAATATAAATATGTTAACGGAAGATACTATCCAGAATGGGGGAGAAAA	716	Qy
788	AWR	729	В
715	ATGCAGTGTAAATTCATTTTACCCCTCCTGACGTAATTACTAGTGGATAGAAAGCGAA	658	Qy
728	AATAAAAAAKAAWRTGKTATAAAAAAAAAAAAAAAARAGGGAKAGGGKRAGARARGGRGGGR 728	669	뮍
657	TACAACACCTACAGTGAAAGTAACGGGTAATGAGTTAGAAGATGGTAACATGACTCTTGA	598	Qy
899	AAAAAAAAAAAGTGTTTGAAGAAAAAAAAAAAAAAAAA	609	Db
597	538 GGGATGTTCATTAGCTATTTTAGATTACCAAAAAATATGGCTAAAAGGTGAAATACCAAAAAGA 597	538	Qy

Search completed: June 15, 2003, 21:36:40 Job time : 1501 secs

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Result
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Listing first 45 summaries
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. /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
. /cgn2_6/ptodata/1/pubpna/US06_EWEP_PUB.seq:*
. /cgn2_6/ptodata/1/pubpna/US06_EUBCOMB.seq:*
. /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
. /cgn2_6/ptodata/1/pubpna/PCTUS_EUBCOMB.seq:*
. /cgn2_6/ptodata/1/pubpna/US08_RFW_PUB.seq:*
. /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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US-09-98-64-761-13293

US-09-764-853A-2

US-09-754-853A-2

US-09-754-853A-3

US-09-790-988-1

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Sequence 7, Appli
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Sequence 9, Appli
Sequence 4292, Ap
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Sequence 5, Appli
Sequence 13, Ap
Sequence 3532, Ap
Sequence 2, Appli
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e ,	Sequence 1. Appli	1 1	1334	μ ω	Sequence 18, Appl	Sequence 2332, Ap	Sequence 3, Appli	Sequence 327. App	Sequence 327. App	Sequence 517. App	Sequence 933, App	e 886	•	Sequence 246, App	Sequence 937, App	88	256	250	70	00	٠.	Sequence 1, Appl	е 1		Sequence 97, Appl

## ALIGNMENTS

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; Patent No. US20020102535A1
                                                                                                                                                                                                                                                                                       Ouery Match 100.0%; Score 1034; DB 10; Length 1034; Best Local Similarity 100.0%; Pred. No. 7.7e-222; Matches 1034; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MCFADDEN, GRANT
APPLICANT: ESSANI, KARIM
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES
TITLE OF INVENTION: FOR IMMUNE MODULATION
FILE REFERENCE: 50082/015002
CURRENT APPLICATION NUMBER: US/09/976,605
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: US 60/239,354
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 9
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                                                                                                                                     GENERAL INFORMATION:
                      CURRENT APPLICATION NUMBER: US/09/976,605
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: US 60/239,354
PRIOR FILING DATE: 2000-10-11
                                                                       TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES TITLE OF INVENTION: FOR IMMUNE MODULATION FILE REFERENCE: 50082/015002
                                                                                                           APPLICANT: MCFADDEN, GRANT APPLICANT: ESSANI, KARIM
            NUMBER OF SEQ ID NOS: 9
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ORGANISM: Yaba-like disease virus
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; ORGANISM: Yaba Monkey tumor virus
US-09-976-605-3
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APPLICANT: MCFADDEN, KARIM
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ANI
TITLE OF INVENTION: FOR IMMUNE MODULATION
FILE REFERENCE: 50082/015002
CURRENT APPLICATION NUMBER: US/09/976,605
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: US 60/239,354
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                   599 ACAACACCTACAGTGAAAGTAACGGGTAATGAGTTAGAAGATGGTAACATGACTCTTGAA 658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 GTAAATTCTAGAGCTTCATGGTTTGATATCTCTAAAAGCCCCTCATACTCCGGGTGACGAT 237
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                                                                                          GGATGTTCATTAGCTATTTTAGATTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGAT 598
                                                                                                                                                        ACCGTTCATGGTCCTAGTTGGCAAACAGTTAAAAAATACGTGGGAGGGTTTGTGTACGCT 537
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                                                                                                                                                                                                                                                                      ACAGGAGATAAAAGGTTTACGAAAATGACACATAAAGGTTTTCCCCAAGGTTGGAATGTTA 478
                                                                                                                                                                                                                                                                                                                                    TCTCTTTTTGGGAGTTACGGATACGTTGAGTCAAGTGGCGGACCGTTGGCTAGGTATAGC 417
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                                                                  GGATGTTTGCTAGCTATTTTTGATTATCAAAAAATGGCTAAGAATAACATACCTAGTAAT
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CURRENT APPLICATION NUMBER: US/09/976,605
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: US 60/239,354
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020102535A1
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                                             207 TTAATATTTCTAGGAGTCCCCACACGCCAGGTAACGATTACAACTTTAACTTTTGGTATT 266
                                                                                                                                   147 CGAAAATATCATATAACCACGAAACTAGACACGGAAACGTAAATTTTAGGGCTGATTGGT 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           779 GATTATGAGCCAGGAGAGCCAGGTTTTCCATGGAATATTAAAAAAAGATAAAGATGCAAAC
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                                                                                        GTTTAAAACTAAATAGCGAGACAGGAAGACCAGAATTAAGAAATGAACCACCAACATGGT 214
                                                                                                                                                                                                                         TAAAAGATAATGGGTTATACGATGGAGTATTTTACGATCATTACAACGATCAGTTAGTAA 146
                                                                                                                                                                                                                                                                        TTACAGCATATGTAGATGCTTCCGCATTCTTAGTATACAATTATACATATACTTTACAAG 94
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                                                                                                                                                                                                                                                                                                                                                            12.9%; Score 133.6; DB 10; Length 1023;
49.0%; Pred. No. 2.5e-20;
ative 0; Mismatches 454; Indels 15; Gaps
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US-10-239-676-30/c
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                                     PRIOR FILING DATE: 2
2000-04-06
2000-04-07
2000-06-30
                                                                                                                     PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058 8
DE 10019173 8
DE 10032529 7
DE 10043826.1
                                                                                                                                                                                                                                                                       APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Disponsis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                   APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
NUMBER
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OF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       861 TACGTACAACATCAAAAATGAGTAGTCAACTAGTATGTGTTTTTCCATGACACTTTAG 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATGACACATAAAGGTTTTCCCAAGGTTGGAATGTTAACTGTAAAAAAACACTCTTTGGA 500
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SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGACTATGTCCTTGACAATTGGATGTACTGATCTAAGACAACTTCAAGTAAATTTCGGTT 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCTGACGTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAGGTGAATATAAATATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGATACAACACCTACAGTGAAAGTAA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGATGTAAAACTTATCTAGGCGGTTTTGAATACATGGGATGTTCATTAGCTATTTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTAGAAACGGCCAACGGACCGTTGGCCAGATACCATACAGGAGATAAAAGGTTTACGA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAGAATGAGTGAAACGCTAGATGAGATAAATAAACTTCCAGAAACGAGTAATCCTTACA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACCAAGCATATAGATGT 945
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                                                                                                        2001-04-06
    228
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; OTHER INFORMATION: chemically treated genomic DNA (Homo saplens) US-10-239-676-30
                                                                                                                                                                                                                                                      ; LOCATION: (1)..(519)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-D1
US-09-878-574-4292
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LENGTH: 7195
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 47.6%;
Matches 131; Conservative
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SEQ ID NO 4292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4292, Application US/09878574 Patent No. US20020110548A1
                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                      Matches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-23(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 1993-06-14
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 519
TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                           FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 TGGAGTATTTTACGATCATTACAACGATCAGTTAGTAACGAAAATATCATATAACCACGA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 AGAAATTAATAAAAACGATAGCACAAAAACTACTT 323
                                   471 GAAIGTTAACIGTAAAAAACACTCTTTGGAAAGATGTAAAAACTTATCTAGGCGGTTTTG 530
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 591 CAAAAGATACAACACCTACAGTGAAAGTAACGGGTAATGAGTTAGAAGATGGTAACATGA 650
                                                                         531 AATACATGGGATGTTCATTAGCTATTTTAGATTACCAAAAAATGGCTAAAGGTGAAATAC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACTAGACACGGAAACGTAAATTTTAGGGCTGATTGGTTTAATATTTCTAGGAGTCCCCA 228
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                          45.5%;
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                                                                                                                                                                                        0; Mismatches 230; Indels
                                                                                                                                                                                                          Score 43; DB 10; Length 519; Pred. No. 3.5;
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Pred. No. 4.8;
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Sequence 5, Application US/09844653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DUFFY, PATRICK E.
APPLICANT: OCKENHOUSE, CHRISTIAN F.
TITLE OF INVENTION: SEQUESTRIN
FILE REFERENCE: 38644-175519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 08/559,896
PRIOR FILING DATE: 1995-11-17
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/351,794A CURRENT FILING DATE: 1999-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                         1191 CCAAAAAAATAAGAAAGAAAATGTAAATGTATTATAATACACGACAATAATGATAGTAA 1250
                                                                                                                                                                                                                                                                                                                                1071 ACTTTATAAAGAAGAATTAGATAGAATGGATAGAGAAGCAAGGTATGAAATCCCCCATGAG 1130
                                                                                                                                                                                                                                                                                                                                                                                                           1011 AATATTACAAGATATACAAAAAGAAAAATACAAAATTTAGAACTAGAAGAAATCGATAG 1070
                                                                                                                              809 TGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGAT 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                569 AAAATGGCTAAAGGTGAAATACCAAAAGATACAACACCTACAGTGAAAG?AACGGGTAAT 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141;
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                                                                                                                                                                                                           AGATACTATCCAGAATGGGGGAGAAAATCCGATTATGAGCCAGGAGAGCCAGGTTTTCCA 808
                                                                                                                                                                                                                                                   AAATTTAAGCAGAAATGAAAAAGATAATATTATACATAGAAATATTAAAAATGAATCTAA 1190
                                                                                                                                                                                                                                                                                      GTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAGGTGAATATAAATATGTTAACGGA 748
                                                                                                                                                                                                                                                                                                                                                                     GAGTTAGAAGATGGTAACATGACTCTTGAATGCAGTGTAAATTCATTTTACCCTCCTGAC 688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1%; Score 42; DB 10; Length 1956; 49.0%; Pred. No. 10;
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.

APPLICANT:

Hanzel, David K.

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US-09-864-761-13293
; Sequence 13293, Application US/09864761
; Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (220202)..(220650)
OTHER INFORMATION: The n at these positions can
NAME/KEY: misc_feature
LOCATION: (222415)...(222416)
OTHER INFORMATION: The n at these positions can
US-09-844-653-5
                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No. US20030054347A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-04-27
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APPLICANT: Rozsa, Frank
TITLE OF INVENTION: Detecting and Treating Eye Disease
FILE REFERENCE: UM-06105
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TYPE: DNA
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LOCATION: (215340)..(215340)
OTHER INFORMATION: The n at this position can
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LOCATION: (203527)..(203963)
OTHER INFORMATION: The n at these positions can
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LOCATION: (122654)..(122654)
OTHER INFORMATION: The n at this position can
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LOCATION: (120172)..(120640)
OTHER INFORMATION: The n at these positions can
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OTHER INFORMATION: The n at these positions can be a,
NAME/KEY: misc_feature
LOCATION: (118272)..(118736)
OTHER INFORMATION: The n at these positions can be a,
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OTHER INFORMATION: The n at this position can be a, c,
NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                        160962 CAGTATGGTTCCAGTGTTCAAAGAAGTTCTTTACACCTATAATGATATGGTTAAGCAAAC 160903
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                   151 AATATCATATAACCACGAAACTAGACACGGAAACGTAAATTTTAGGGCTGATTGGTTTAA 210
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                                                                                                                                                                                                                                                                                                             91 AGATAATGGGTTATACGATGGAGTATTTTACGATCATTACAACGATCAGTTAGTAACGAA 150
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Similarity 51.6%;
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Pred. No. 1.1e+02;
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APPLICANT:

Chen, Wensheng

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OTHER INFORMATION: MAP TO ACO12404.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2

US-09-864-761-13293
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13293
LENGTH: 563
                                                                                                                                                                                                                                                                                                        Query Match
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/774,203 PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
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PRIOR APPLICATION NUMBER: GB 24263.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/180,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                      Local
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(APPLICATION NUMBER: PCT/US01/00667
OFFICING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
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APPLICATION NUMBER: US 09/632,366
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/234,687
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1015 AGAAGACGGAAA 1026
                                                                                                               112 AATAAAATAATTCTTAAAAATGTAAAGGATGGAAAAATGTAAAGGATGAATTAAAACAGT 171
                                                                                                                                                                                                                             835 AAACACATATAGTTTAACAGATTTAGTACGTACAACATCAAAAATGAGTAGTCAACTAGT 894
                                                                                                                                                                                                                                                                    98;
                                                                                                                                                                                                                                                                                    Similarity
                                                                         TGGAGAGCTATACGACCACCTATATAGAAAAACAGAAGGAGAGGAGAAGGTGAAGAGGATGA 1014
                                                                                                                                                   ATGTGTTGTTTTCCATGACACTTTAGAAGCGCAAGTTTATACTTGTTCTGAAGGATGCAA 954
                                       Conservative
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                                                                                                                                                                                                                                                                                    4.0%;
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                                                                                                                                                                                                                                                                  Score 41.6; Di
Pred. No. 7.4;
0; Mismatches
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US-09-938-842A-3532
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                                                                                                                                                                                                                        Sequence 190, Application US/10239676 Publication No. US20030082609A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR PILING DATE: 2000-08-24
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                    APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.103
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-06
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                               APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Arabidopsis thaliana
PRIOR APPLICATION NUMBER: PCT/EP01/03968
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Local Similarity 45.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 CATAAGAATTGAACAAAATGATTATGGTAAATGGTAACCAAAAAGGTGAACTAATATTTA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482 AAAGTTCTGTATGAATTTAAAATAAATTAAATTATAAATTTCTCTTCAAAACATTTATTT
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 Mismatches

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US-09-754-853A-2/c
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                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Soybean Cyst Nematode Resistance FILE REFERENCE: 38-10(1581)8 CURRENT APPLICATION NUMBER: US/09/754,853A CURRENT FILING DATE: 2001-01-05 PRIOR APPLICATION NUMBER: US 60/174,880 PRIOR FILING DATE: 2000-01-07 NUMBER OF SEQ ID NOS: 1119 SEQ ID NO 2
LENGTH: 335913
                                                                                            Query Match
Best Local
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SEQ ID NO 190
LENGTH: 6204
TYPE: DNA
                                                                           Matches 142;
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APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
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2000-04-06
                                                                                                                                                      NAME/KEY: CDS
LOCATION: (45163)..(45314),(45450)..(45509),(46941)..(48763),(48975)..(49573)
OTHER INFORMATION: Clone ID: 240017_region_G3
                                                                                                                                                                                                                                         ORGANISM: Glycine max
                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                          FEATURE:
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Match 3.98;
Local Similarity 50.88;
                                                                                            Local Similarity
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10019173.8
10032529.7
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                              5 TTCATGAATAAGTTAATATTATTTAGCACAATTGTAGCAGTTTGTAACTGCATAACTTTA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAGCTATTTTAGATTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGATACAACACCT 607
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                                                                           Conservative
                                                                                        3.9%;
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                                                                       Score 40; DB 9; Length 335913;
Pred. No. 2.7e+02;
0; Mismatches 170; Indels 0
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Pred. No. 44;
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Sequence 3, Application US/09754853A
PUBLICATION NO. US20030005491A1
GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
APPLICANT: Parsell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And TITLE OF INVENTION: Soybean Cyst Nematode Reprication Application UNMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
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; LOCATION: (46798)..(48763).(48975)..(49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-3
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US-09-754-853A-3/c
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LENGTH: 335913
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Best Local Similarity
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ORGANISM: Glycine max
FEATURE:
280270 AATATTATATCTTTTAATCAGCCTATTATTAATAATAGTTTTGATACATAAATTTAAAT 280211
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                                                                                    280330 ATGAGATTTATATATAATAAATATATATATACTAATACTAATTTATATATAACATATATAT
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                                                                                                                            185 GTAAATTTTAGGGCTGATTGGTTTAATATTTCTAGGAGTCCCCACACGCCAGGTAACGAT 244
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                                        245 TACAACTTTAACTTTTGGTATTCTTTAATGAAAGAAACTTTAGAAGAAATTAATAAAAAC 304
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Pred. No. 2.7e+02;
0; Mismatches 170;
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280210 TATAAAATTAAA 280199

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US-09-790-988-1/c
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; TYPE: DNA
; ORGANISM: Buchnera
US-09-790-988-1
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                                              Matches 180;
                                                                                          Query Match
                                                                                                                                                                                                                       SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local Similarity 52.8%;
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                                                                    Best Local Similarity
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SEQ ID NO 1
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APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR PPLICATION DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
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APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
CURRENT FILING DATE: 2001-02-3
                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SHIGENOBU, SHUJI APPLICANT: WATANABE, HIDEM
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PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                   LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera sp.
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                                                Conservative
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                                                                  43.5%;
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Pred. No. 3.7e+02;
""Asmatches 77;
                                            Score 39.6; DB 10;
Pred. No. 4.1e+02;
0; Mismatches 234;
                                            Indels
                                                                                     Length 640681;
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347004 TGTCAGGATCACGATTTGTTATAATGAAGGGAAAAATTGCTCTTTTACACCGTG
                                                                                                            347064 AAGATCATATAGAGCTAGGAAAAAATTTAACGAATTAGATTGGAAATCTTCTGCACAAA 347005
                                                                                                                                                                                                                                                                                                                                 347184 ATCATTTTTCTATGTGCATACCTAATATTCCTTCTGACGATGTTCCAGAGGGAAATACAT 347125
                                                                                                                                                                                                                                                                                                                                                                                                                                                 347244 AGTCAAGTAAAGATTTAAACGCTTCTAAAATTGAACTTAATTCTTTAAAAGAAAAAATAC 347185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347304 TATTTAAAGAAAACAAAAATATTAAGAATAAAAATGAATTGTTAAGACATCAAGTTATAC 347245
                                                                                                                                                                                                                                                                                                                                                                                               678
                                                    858 TAGTACGTACAACATCAAAAATGAGTAGTCAACTAGTATGTGTTGTTTTCCATG 911
                                                                                                                                                             798 CAGGTTTTCCATGGAATATTAAAAAAGATAAAGATGCAAACACATATAGTTTAACAGATT 857
                                                                                                                                                                                                                                                           738 ATGTTAACGGAAGATACTATCCAGAATGGGGGAGAAAATCCGATTATGAGCCAGGAGAGC 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     618 TAACGGGTAATGAGTTAGAAGATGGTAACATGACTCTTGAATGCAGTGTAAATTCATTTT 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       558 TAGATTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGATACAACACCTACAGTGAAAG 617
                                                                                                                                                                                                                     CGATTAATAAAGAAATTAAATACTGGGGTCAAAAAAAAGAAGTATGATTTTGAAATCC 347065
                                                                                                                                                                                                                                                                                                                                                                                            ACCCTCCTGACGTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAAGGTGAATATAAAT 737
346951
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Search completed: June 15, 2003, 21:41:34 Job time : 194 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1034
1 aagcttcatgaata
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10958.595 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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1: gb_ba:*
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gb_ph: *
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em_htgo_hum:*
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Pred. No. is the number of results predicted by chance to have a

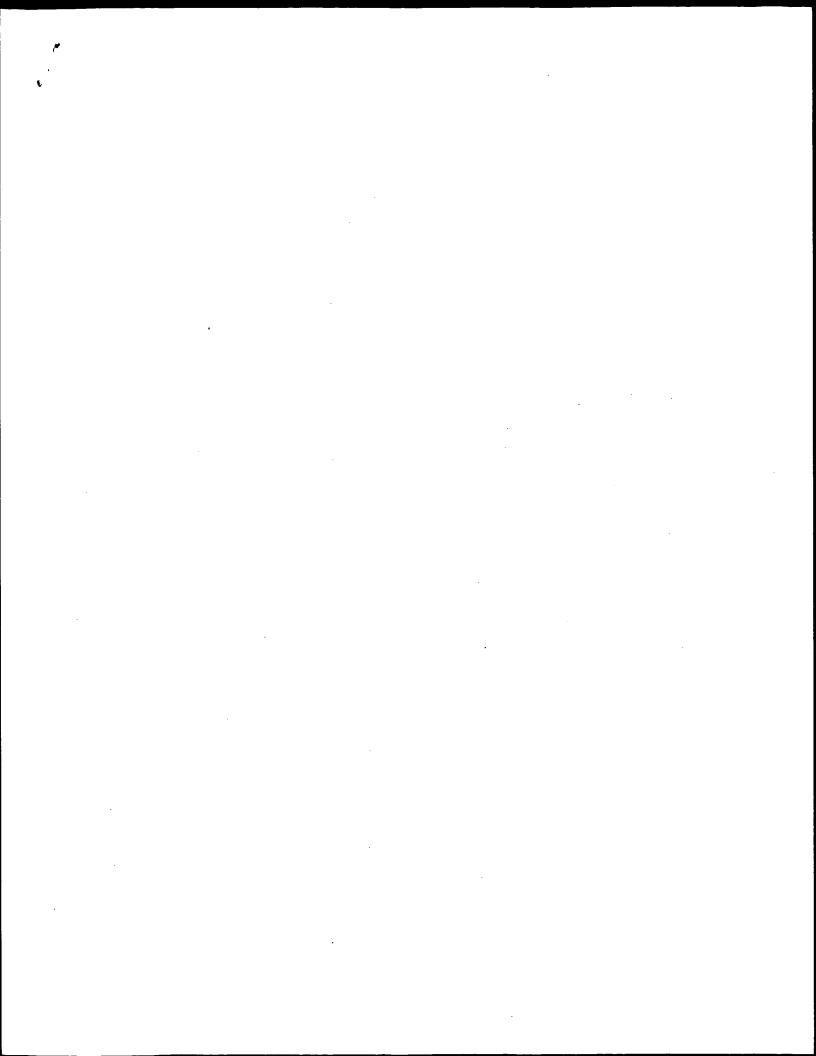
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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AC112577 Rattus no	344559 Sequenc	79	۳.	P.falcipa	6	Seguer	900	77 R	ہۃ	Plasmo		AX346209 Sequence		E08995 DNA encodin		32	AC116330 Dictyoste	57		, P	u	-	ω.		٠.	3744 5	93805	ACIIO936 DICTYOSTE		166494 Sequence 14	3 Swine	3 Swinepox	13 Swinerce	TS8397 Sequence 1	o company	570 Sequenc	727	JID Sequence by	45601 Sequence	293568	Description		

# ALIGNMENTS

	VERSION KEYWORDS	RESULT 1 YD1293568/c LOCUS DEFINITION ACCESSION
1106L gene; 1117L gene; 117L gene; 122R gene; 128L gene; 133L gene; 139R gene; 144R gene;	AJ293568.1 100L gene;	YDI293568 Yaba-like (
107L gene; 111L gene; 118L gene; 123R gene; 129R gene; 134R gene; 13L gene; 145R gene;	GI:12056159 101L gene; 1	YDI293568 144575 bp DNA lines Yaba-like disease virus (YLDV), complete genome
108L gene; 112L gene; 119L gene; 124R gene; 12L gene; 135R gene; 146R gene;	59 102R gene;	144575 bp us (YLDV),
109L gene 114R gene; 11L gene; 125R gene; 130L gene; 136R gene; 141R gene; 147R gene;	103L gene	DNA complete go
; 10L gene; ; 115R gene; 120L gene; ; 126R gene; ; 131R gene; ; 137R gene; ; 137R gene;	; 104L gene	Ħ
107L gene; 108L gene; 109L gene; 10L gene; 11/3R gene; 111L gene; 112 gene; 114R gene; 115R gene; 116R gene; 118L gene; 111L gene; 111L gene; 111L gene; 111L gene; 120L gene; 121L gene; 121R gene; 127R gene; 123R gene; 124R gene; 125R gene; 126R gene; 127R gene; 129R gene; 121L gene; 130L gene; 131R gene; 1	; 105L gene;	VRL 30-MAY-2001



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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; 3L gene; 4Lu gene; 4LL gene; 4EL gene; 4AL gene; 4SI gene; 4GL gene; 5R gene; 5GR gene; 5R gene; 6GR gene; 7GR gen
                                                                                                                                                                                                            Submitted (13-JUL-2000) Lee H.J., Pathology, University of Oxford; ;
                                                                                                                                                                                                                                                                                                                                                                                                                           Thesis (2000) Sir William Dunn School of Pathology, University of Oxford, Oxford, UNITED KINGDOM

2 (bases I to 14457ED KINGDOM)

Lee, H.J., Essani, K. and Smith, G.L.

The genome sequence of Yaba-like disease virus, a yatapoxvirus Virology 281 (2), 170-192 (2001)
                                                                                                                                                                                                     UNITED
                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                           Lee,
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Yaba-like disease virus
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                                                                                                                                                                                                  KINGDOM
complement(755. .1756)
                                                                                     /organism="Yaba-like disease virus"
                                                                                                                                                          Location/Qualifiers
                             db_xref="taxon:132475"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                            South Parks road,
                                                                                                                                                                                                                               Sir William Dunn School of
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                                                                                                                                                                                                                                                                       strain Copenhagen N2L*
                                                                                                               /product="4L protein"
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                                                                                                                                                                                                                                                                                                                                                                         complement(3630. .4346)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3630. .4346)
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                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                citation=[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="31 protein"
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/gene="3L"
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                                                                                                                                                                                                                                                                                                                                         function="Unknown"
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/gene="2L"
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/gene="2L"
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PUBMED REFERENCE

MEDLINE JOURNAL AUTHORS

AUTHORS TITLE

REFERENCE

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JOURNAL

AUTHORS

TITLE

FEATURES

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VGIFLEEPLOCTFYTIQLISKSIMNKQEVLEIMSELKKDNYYFENIFYTTIFDHHLYD
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                                                                                                                                                                                                                                                                                                                                                                                                                   'note="related to swinepox virus C5L and vaccinia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKINLYEMFNGDPINYCKYSIGFYSILFDYFPLYYNFDTDFFNQVSIRYRMILKEELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="related to swinepox virus C5L and vaccinia virus
strain Copenhagen K7R"
/citation=[2]
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EDRHRGREYTLVLHLSSPKNGGKTDVCYGDKTYLSTADDFLLEKRSEQLSNVVQEGEK
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EDLWYPSSEEDYKFLRELVDYYSSNLKTKVDYYVLSTCDDDETQYVSLNVIRCYFSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:Q9DGU2"
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TAACTTTAACTTTTGGTATTCTTTAATGAAAGAAACTTTAGAAGAAATTAATAAAAACGA
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SLAEYWGGEDLFTNDSLQALKLMTILLSDDDYSFIDLCLRVRLKKLK*
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/gene="5L"
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Moyer, R.W., Vinuela, E. and Gibbs, E.P.J.
Use of recombinant swine poxvirus as a live
Patent: US 6217882-A 53 17-APR-2001;
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AR145601
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Score 133.6; DB 6; Pred. No. 9e-16;
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Matches

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#### STIC Database Tracking Number: 96300

TO: Ulrike Winkler

Location: cm-1/8d09/8e12

**Art Unit: 1648** 

Monday, June 16, 2003

Case Serial Number: 976605

From: Mona Smith

**Location: Biotech-Chem Library** 

CM1-6A01

Phone: 308-3278

mona.smith@uspto.gov

#### **Search Notes**

Thank you for using STIC services
Feel free to contact me if you have any questions.

Mona Smith 308-3278



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#### STIC-Biotech/ChemLib

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From: Sent: To:

Winkler, Ulrike Tuesday, June 10, 2003 3:53 PM STIC-Biotech/ChemLib

STIC,

Please search SEQ ID NO 5 of application 09/976605.

Thanks, Ulrike

Ulrike Winkler, Ph.D.
Patent Examiner
Crystal Mall 1, 8D09/ Mail Box 8E12
1911 South Clark Place
Arlington, VA 22202
tel. 703-308-8294
fax. 703-308-4426

Searcher: M. Sm. 771
Phone:
Location:
Date Picked Up: (6しい 8 3
Date Completed: 6116103
Searcher Prep/Review: 3
Clerical: 5
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (w	here applic.)
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Other (specify):	

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### STIC SEARCH RESULTS

### **Biotech-Chem Library**

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

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>	I am an examiner in Workgroup: Example: 1610								
>	Relevant prior art <b>found</b> , search results used as follows:								
	☐ 102 rejection								
•	☐ 103 rejection								
	☐ Cited as being of interest.								
	☐ Helped examiner better understand the invention.								
	Helped examiner better understand the state of the art in their technology.								
	Types of relevant prior art found:								
	☐ Foreign Patent(s)								
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)								
>	Relevant prior art not found:								
	☐ Results verified the lack of relevant prior art (helped determine patentability).								
	Results were not useful in determining patentability or understanding the invention.								
C۵	Comments:								

Drop off or send completed forms to STIC/Blotecht Chemillbrary CM1 - Circ. Desk



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#### Winkler, Ulrike

From:

Winkler, Ulrike

Sent:

Tuesday, June 10, 2003 3:53 PM STIC-Biotech/ChemLib

To:

STIC,

Please search SEQ ID NO 5 of application 09/976605.

Thanks, Ulrike

Ulrike Winkler, Ph.D. Patent Examiner Crystal Mall 1, 8D09/ Mail Box 8E12 1911 South Clark Place Arlington, VA 22202 tel. 703-308-8294 fax. 703-308-4426

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